



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/1073,605
Source: PCT09
Date Processed by STIC: 2-27-2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
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Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
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2011 South Clark Place, Arlington, VA 22202
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Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Does Not Comply
Corrected Diskette Needed

See page 10



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,605

DATE: 02/27/2002

TIME: 13:33:36

Input Set : A:\Ep.txt

Output Set: N:\CRF3\02272002\I673605.raw

4 <110> APPLICANT: The President and Fellows of Harvard College
6 <120> TITLE OF INVENTION: REGULATION OF BIOFILM FORMATION
9 <130> FILE REFERENCE: 00246/505WO3
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,605
C--> 11 <141> CURRENT FILING DATE: 2000-10-17
11 <150> PRIOR APPLICATION NUMBER: 60/102,870
12 <151> PRIOR FILING DATE: 1998-10-02
14 <150> PRIOR APPLICATION NUMBER: 60/083,259
15 <151> PRIOR FILING DATE: 1998-04-27
17 <160> NUMBER OF SEQ ID NOS: 49
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

ERRORED SEQUENCES

21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1090
23 <212> TYPE: DNA
24 <213> ORGANISM: Psuedomonas fluorescens
26 <220> FEATURE:
27 <221> NAME/KEY: variation
28 <222> LOCATION: (1)...(1090)
29 <223> OTHER INFORMATION: n is a, t, c, or g.
31 <400> SEQUENCE: 1
E--> 32 gagegcagna gaggaagn gn gggagganga ggaaggagga gagnggaaga aggggggaag
W--> 33 60gggagggggg aaggagagn ggggagnngg gggnatnngg gannngggng gggngnggnn
W--> 34 120ntgnttatna tnangetccg gccggacgaa gaaattcccg atgcattgct cgagcgcgta
W--> 35 180ggcctgtctc gggacaaggt caaccacgta ttcagcaaag tgctcnaggc ggaantgctg
W--> 36 240ctgcgcgaac tggcctcgca nttagccac ggctgaatag gctcgcccgg tcatattgatc
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W--> 38 360aacgeggagc gtccctggcg acnttccnc ncaggagcg tggggaacn ancaaantg
W--> 39 420gtccctcga ttntaaagt cttecttaa ancttcttnc gggttccag ggtattttgg
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W--> 42 600ttttgtttcc ctttgggccc ntncaatcc gntgnggcaa aaacgccat tanggggcn
W--> 43 660ggcggtgcc ccccccnng nntgttactn aantncanaa cgccnnttg gccanaaann
W--> 44 720tcgncngng nnnnnncnc gncnttttn ctnccttcc nnnctntnt cctcngtgta
W--> 45 780tntccaantc ntncnncgc centcngcc tccccactnc ctngccctc cnnncnncg
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W--> 47 900nnnnngtca tcnntgncgc tcttccnccc nccctgtcn cccantgcn ngnnctcgc
W--> 48 960aggtegcnng tetencncc nccngnttcg tgennggn cnngatcccg ttcnncnng
W--> 49 1020ncntnatgc tgaccagtnn gngngngtng nnnctcccg tcngnacntg tntngngggg
E--> 50 1080gggccnccc

1090

Numbering of nucleotide
sequence must be to the
right of each line. See
37 CFR 1.822 (c)(1)-(7). Also,
see sample provided
at back

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Input Set : A:\Ep.txt

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52 <210> SEQ ID NO: 2
53 <211> LENGTH: 277
54 <212> TYPE: DNA
55 <213> ORGANISM: Psuedomonas fluorescens
57 <220> FEATURE:
58 <221> NAME/KEY: variation
59 <222> LOCATION: (1)...(277)
60 <223> OTHER INFORMATION: n is a, t, c, or g.
62 <400> SEQUENCE: 2
E--> 63 gnggggngng ggncttgtgt ataaatntca ggctctgaca tccaggccgc aggcggcctg
W--> 64 60gtcccnatgg ttatcgacca ntccgcccgc ggcnangtg cctatnanat ctactcncgt
W--> 65 120ctgtctcaang aacgcgtcat ctttctggtg ggcccggtaa aagactacat ggccnacctg
W--> 66 180atctgtgcgc aactnttggt ccttgaancc naaaacccgn acnaggatat ccatctctat
E--> 67 240atcaacnccc cnggtactag ttcaaccctg gaaaaaa
277
69 <210> SEQ ID NO: 3
70 <211> LENGTH: 819
71 <212> TYPE: DNA
72 <213> ORGANISM: Psuedomonas fluorescens
74 <220> FEATURE:
75 <221> NAME/KEY: variation
76 <222> LOCATION: (1)...(819)
77 <223> OTHER INFORMATION: n is a, t, c, or g.
79 <400> SEQUENCE: 3
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W--> 81 60ntccattgga tgaatgtcca cccgtccatc cnancctgga agccaggatt nctgcccgc
W--> 82 120atnanggtnc ggggtggcaac aatctcaccg naacctgnnc ctgtgggtcac aancgaggtt
W--> 83 180caggtcacca cggncgtccc ggcaccggtt gccccnctgg tcaggccggg ccagggnncg
W--> 84 240gtngccccag angtcnatcc tccctttgac cctnaancng acccgcnena tgctggcna
W--> 85 300ccnttgcntt tggcaatgga ccngggngga catnttnccg cccgtatcc agggcnenc
W--> 86 360ccaanantac ngccccggcg tccctctann ntntactatt cnaecgtgg gcananntgc
W--> 87 420ccctngtngg cttncccttc tcttcccogn cncctntttt tcccnnttt ttttgnccg
W--> 88 480gncnctct ctnctcctnc ctccnncnnn cntcgtctn nnnccctngt gggcctcnc
W--> 89 540cctttntcct tcttccnncn tttntctccg tggccctnct ctctgnttcc ncnngtngc
W--> 90 600gtccgggtan cccagcctcg ctctccnccg ctgmngcnct ctentttctt gcttctctt
W--> 91 660ccctgtggcc ctntgcgac ncnncanctt ctctcgtctn nggtcnanc cttngtntc
W--> 92 720cgcnngngnc gnncnctnc tctngcnccn nnntcgtctt cgtnnncnng tctnnnnn
E--> 93 780ncagtcnngt gtngnnagnt tnnccnagtn tgnnatccc
819
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 832
97 <212> TYPE: DNA
98 <213> ORGANISM: Psuedomonas fluorescens
100 <220> FEATURE:
101 <221> NAME/KEY: variation
102 <222> LOCATION: (1)...(832)
103 <223> OTHER INFORMATION: n is a, t, c, or g.
105 <400> SEQUENCE: 4
E--> 106 gatggtatcg gtnactcggg caccgctggg gtggtgctcg gaacagggtc tcgaagttcc
W--> 107 60cgccagtggc cttatcgatg ctgacttcaa ctttgcccgc gtctttgtag acgtcgtctt
W--> 108 120ttggtgcgtc gacagtcacg gtgccggtcg tggcgcccgc agcgatgttg atcaccgcgc

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W--> 109 180cgttgctcag ggtcacagtg acaggcgagc cgcggcggtt ggtcaagggtt gcggtgtaaa
W--> 110 240cgatcgaacc gccttccgca acgctatcgg ttgcactcaa agtcaggccg gtagtgctct
W--> 111 300gaatgtctgt nanngtggtg tcngecgggg tggegtccan gtccaatatt tcataattnc
W--> 112 360nacntggggg tcttccannt tnanntcaa gttatcgccc cccccaaag gctccttng
W--> 113 420cgtnacnaaa ttcaccgann cegantggc nccnaaccgg aanggtgang gtctggggccg
W--> 114 480ttcnaacang gttnnataac caaacggaac ntcgggtcac cggtttctnt taacngaagg
W--> 115 540nggtgttnna accncggnc cnccttccgg ccaangngng aaattnnng gtggnggaa
W--> 116 600aanaggctna ngttttnaan gggtttccng tnancntent nnncccnan ggntttntn
W--> 117 660ntnanaaacc aaanntcncc ngaatttncc nccnggtngg nttttnnng nanngngaa
W--> 118 720ntnnnggggt gggnnnnccn ntcctttgtt tnnaaaatna nncntttng ggnccnnnc
E--> 119 780naaaaggngc annngnggnc cnnntgggnn ggnnnccnnn gggncnaag nt

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832

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121 <210> SEQ ID NO: 5
122 <211> LENGTH: 1054
123 <212> TYPE: DNA
124 <213> ORGANISM: Psuedomonas fluorescens
126 <220> FEATURE:
127 <221> NAME/KEY: variation
128 <222> LOCATION: (1)...(1054)
129 <223> OTHER INFORMATION: n is a, t, c, or g.
131 <400> SEQUENCE: 5

```

```

E--> 132 cncaanggen cagagcacag gatatgengc aatctcatgg acaaacggcg ccagcccnat
W--> 133 60ggaggccacc gacnccacat cgtcgcgcc ggtcgttgc aggcncgcc acgcancctc
W--> 134 120aaggttctgc gccanttga ncnctnctc gncaccanc cnnagttgc agcncncaa
W--> 135 180actccccacc ncnannnc ntnacnaaat nntgggttc cgnataccgc cncactcac
W--> 136 240gcaccaattg ctcaccncg gctgaacna actggtcggg ncnctnccg cccatccnc
W--> 137 300tggttnaaac nggcnattc cttnaccccc agcaacancn aataaccgg acctggccan
W--> 138 360cnccgggtng ctcaccggg cattaaactg cattttcaa atatnccgg ttggccacgc
W--> 139 420ccgtnagggt gtcctgntag gatecnacc ccantttnc tntgcccctn ggnetgntn
W--> 140 480nggaannngn centgagctt tctcgacct ctgggtttct tntctngcn cccactncg
W--> 141 540nnncaagttt taaggtntn nctccgggna atcctctnng gcnannnctt naactgnaaa
W--> 142 600cttccnccga acngggncct aanantagnc ctatnngggg nnacnngcgt tgnccaaccn
W--> 143 660aactnttttt ttttccagc cgcggggctn ttcaagtent tgaacgnaac tctcnngtc
W--> 144 720nttccacang gntcccccc tantntntaa ccgctntcn tctatnttgg gngtccccgn
W--> 145 780ntncatacat gncngagtan aagaagcten ancctccna nnnngntctc cgcgcccaa
W--> 146 840tttntccct ctctccctt nancntctaa atatattctt tnntgggnnt naanaagggg
W--> 147 900ggcgcanaaa nacctntctc cggggggggt tgtgggncct nnanaaacc cctttctnt
W--> 148 960tntnnncccc cctcggngg ggtccnccc tccctntttg tttccccc ctannaatcc
E--> 149 1020ctactcnng gnetagttga aaaaacanna acgc

```

1054

```

151 <210> SEQ ID NO: 6
152 <211> LENGTH: 880
153 <212> TYPE: DNA
154 <213> ORGANISM: Psuedomonas fluorescens
156 <220> FEATURE:
157 <221> NAME/KEY: variation
158 <222> LOCATION: (1)...(880)
159 <223> OTHER INFORMATION: n is a, t, c, or g.
161 <400> SEQUENCE: 6

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```

E--> 162 ncnnacgnnt ngnaagtgat caggccnatt aaacnnntga cnaaannaga acangnnggt
W--> 163 60ctgttactac ttttcaagac caacccaagn cgaccgtgna tagcngncc tntacgcagc

```

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W--> 164 120atcngttccn catttagatt nntatccatc cntaagtttc nccgggtcag aacgntnctt
W--> 165 180gacgtacaac ccatanngeg gggtannggg nnatttttng ctacctcnca tgttttggaa
W--> 166 240gncnancntnc cntttaatng gnagcnnan ncangcncnn ggggattatt acnactcnac
W--> 167 300ccntgganaa cnttgccact acngcnggnc ccccgcnng tccnggnctc cccgtgcccac
W--> 168 360ttcccttgte tcccgncctc tntnccccct tttcncgtcn ncttctgggtg tncgnttccc
W--> 169 420ctccccccng tccctnttca ncnctnngcg tctngggcac ctngncgnnc tcttccctnc
W--> 170 480tgggccctct ncccccentt cgttntance cctctctcna cntncttcat cccgtccctn
W--> 171 540ttcttntctet ccnctcncn cccntnctta ntccntnctg cccnctnctn tcntcgtctn
W--> 172 600cctnncncnc ttntcgactt cnnctngttg nccccccgc ngngncttct ctngtcttct
W--> 173 660cccgctngcn gctcagncnc cntccttccn ttntnctnn ctgtccgncn gcgnnctgt
W--> 174 720nccnecgncc cctagnnngg ncgcgcctcn gcnnccctgt cccnngntnt nntctttctg
W--> 175 780cncctgtctc nntnttctn tntcnnctcg cccatccnct nccctctnnt nncgtngtt
E--> 176 840ccncttctag gncnncattc cnannncngg ccnttncccc

```

880

```

178 <210> SEQ ID NO: 7
179 <211> LENGTH: 779
180 <212> TYPE: DNA
181 <213> ORGANISM: Psuedomonas fluorescens
183 <220> FEATURE:
184 <221> NAME/KEY: variation
185 <222> LOCATION: (1)...(779)
186 <223> OTHER INFORMATION: n is a, t, c, or g.
188 <400> SEQUENCE: 7

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E--> 189 ncaanncaga tcttgnaaaa cgggaaaggt tccnttcagg tacgctactt gtgtataaaa
W--> 190 60gtcaggggccc aaacgcccc ggtgcaacaa ctggtcnaag gctacntggc ggggtacaac
W--> 191 120cgtgcgctgg tcnaacgcaa ggccaaaggc ctgcccnaac aatgtgccag cnaatgggta
W--> 192 180cggccgatca cggcgctgga cctgggtcaag ttgaccgccc ggctgttggt ggaagggggc
W--> 193 240gtcggccagt tcgcccangc cctggccggc gcgcaaccgc cccaggcnac cgcactcgcg
W--> 194 300ggcaccgccg tcaccggttt cgcggccgcc gcaaccgccc agcagcnttt tgccctgaaa
W--> 195 360cgcggcaaca atgcnttggg ccacggtcan cnaacgctcg ttcaatgggc cgttnggaat
W--> 196 420ntttgcttgg caaaccccc atttttcccg ttgggttagg cggcattcct tttctnacca
W--> 197 480naaagcacct gaaccattcc cgggcaanct tggaaattct tgggccccng ngcctgccaa
W--> 198 540ttttgccnaa aaatcaanat cggtttcaac canccnctt gcctggaacc aaaccgtcaa
W--> 199 600aaactccaaa aaaattcccc cttnccnctt gcaatcnntc naagaaccaa cctttttttn
W--> 200 660ccaaggnatt ttttttccna naaacmcaa angtnnttnt naattttacn acttaaggcc
E--> 201 720anttnnaaag tncccaattt tttanngtcc aatttgnccc nattttaaag gctccggtt

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779

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203 <210> SEQ ID NO: 8
204 <211> LENGTH: 848
205 <212> TYPE: DNA
206 <213> ORGANISM: Psuedomonas fluorescens
208 <220> FEATURE:
209 <221> NAME/KEY: variation
210 <222> LOCATION: (1)...(848)
211 <223> OTHER INFORMATION: n is a, t, c, or g.
213 <400> SEQUENCE: 8

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```

E--> 214 gccnnnnncn nattatncaa gntctaagtg ttinnaccana tnccaaggac ataatgactt
W--> 215 60nccctttatta antgtccgga ccatnccata tncaaccgtg canaccgtna acttnacca
W--> 216 120ncatgnetcc gentgtcgta tttatanncc ccataagctt cnccegtcag aacgttncaa
W--> 217 180taggtacant natactgcn ggcnatggc attttgctt tctttatgtt nggnagtctn
W--> 218 240aacagccttt ttatggagcg tccacagcta tagggggaaa ntntctattca acnctggcna

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W--> 219 300aanttttga aaactnaganc ttcnnnggtn tataggggta tcccntgacc aaannccnct
W--> 220 360aattccnacb ctttgntccc acttctctcc tngcgcgnet ttaccnngng ccccgteccet
W--> 221 420tccccnengn ncntnggnca cngggggaaa ngnnntcncc ccgtggtttt ctcccnngtn
W--> 222 480tngnnnnncc tegtgnntcc cggnnccctn cccccngtt cggaaactnt ctccctctcn
W--> 223 540cccnccgng tgcgtctnnn tnncccnngn tncnnggnt tncnngcnc cctttctctc
W--> 224 600cccccccccc ttanccngga nccctctccc tncgcntggc cngccccccn ggnccctccc
W--> 225 660ctntnccctc gngnncncc gncgncctcc ttncnttcg cctctccnn cctcnctc
W--> 226 720cncctncc nntcccncc ctctnnntc cccntgccc nnnncnccgg ccttcgntc
W--> 227 780ctcnnnnnnn tncctgngcc cgcgtgcnch gtngcgnccc gctntcctgc ctgtcncccc
E--> 228 840ccctnccc

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848

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230 <210> SEQ ID NO: 9
231 <211> LENGTH: 533
232 <212> TYPE: DNA
233 <213> ORGANISM: Psuedomonas fluorescens
235 <220> FEATURE:
236 <221> NAME/KEY: variation
237 <222> LOCATION: (1)...(533)
238 <223> OTHER INFORMATION: n is a, t, c, or g.
240 <400> SEQUENCE: 9

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```

E--> 241 tatttggtga taagntcagc gccagcagtg accgatgtca ccgataccat cgacaccagc
W--> 242 60accgtttcgc tcacagcgac ttcgacggtg gccgaagggt ggactgtcgt ttacaccgcc
W--> 243 120tcggttaacg caccctgac cgacgtccg ttggttatca cctgttcca aacggccana
W--> 244 180ccatcnccat tccggttggg gccagcanch gcaccgtgaa cttcgtgaca ccaacgcag
W--> 245 240ccctcgcggg cggcgataac ctgagcgtga agattgatga cgccaagggt ggcaattacn
W--> 246 300aaaaactgga catcgacgcc accccggcgg acaccaccgt taccgatntg caggacacta
W--> 247 360ccggcctgac cttgantgca accgatagcg ttgctgaang cggntcgatc gtttacaccg
W--> 248 420caacattgac caacgcncncc ggntcgctg tcnctgtnac cctgaacaac ngngcgggtga
E--> 249 480tcaacatccc tgcggnggtt tcccccccg tntantcta cacgngngaa aaa

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533

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251 <210> SEQ ID NO: 10
252 <211> LENGTH: 591
253 <212> TYPE: DNA
254 <213> ORGANISM: Psuedomonas fluorescens
256 <220> FEATURE:
257 <221> NAME/KEY: variation
258 <222> LOCATION: (1)...(591)
259 <223> OTHER INFORMATION: n is a, t, c, or g.
261 <400> SEQUENCE: 10

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E--> 262 tgattgtgta taagatcagc cagcaaggcg ccgtcgtcgg gttggtaaag cccaccagc
W--> 263 60aacttggcca ggaactctt gcccgagccg ctgcggccaa tgatgcnat tttctgccc
W--> 264 120ggcttganca ccaggttnat attctacacc tngggnttct gctgggtcgg anaatnaaa
W--> 265 180nttcaactna nngnattcca acggccctt ccagaacttt cnggtcangg gngctcnc
W--> 266 240caaattgcgc tcttggggca gtcctcat ctggtcgana ganatcttgg tcccccccc
W--> 267 300ctgttggtat cgggtcntca ngcccnacaa cnaaaccaac nggctgagg cgcgaccgt
W--> 268 360gaacatntnt cangcgacca nccccccnt gctcangcna ccggcgatna tcaagtntac
W--> 269 420nccnaaaana anatgaccac cccngccagt tncgtgatca acaaagtgat gttctttgcc
W--> 270 480nggccggana acatcttcac ccccanttct aagcggctga aggtgccgat agtctgttcc
E--> 271 540cncgtgttatt ggcgtncncc ccccntact antcaacnch tggnaaaaaa a

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591

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273 <210> SEQ ID NO: 11
274 <211> LENGTH: 1249

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275 <212> TYPE: DNA
276 <213> ORGANISM: Psuedomonas fluorescens
278 <220> FEATURE:
279 <221> NAME/KEY: variation
280 <222> LOCATION: (1)...(1249)
281 <223> OTHER INFORMATION: n is a, t, c, or g.
283 <400> SEQUENCE: 11
E--> 284 ctgggtgtat aagatcaggg ccantngtgt cctggagtgt ctgtnacagt gggttcggca
W--> 285 60ngcttgccct cnanatncan tttttcgtaa ttgccaccct atggcctnct ccnaatttga
W--> 286 120ancacnaggn acctncccan tgncaagggc ttcttcngcn tcnngaaatt canccnacnn
W--> 287 180naaatngggc caacctgan tggttaccgt cntgccgenc ccnctcnggn catttctctg
W--> 288 240ccnaagcntc ccggtncctn gnttgcttc taacccaagc gncngntntn nancnncctt
W--> 289 300gtttcncccc tncngncna cgggtggaan ggttttncce centaggggc ctcnnttttt
W--> 290 360tctaaancgc tttccagaa aaaggcctgc ccggtntacn cttcttann tntcgtcgcg
W--> 291 420tccnagngct tctnctctc tnncccttc ggatactnct ctgtaagttt ccctaaaatc
W--> 292 480nctgngntng gnttctnnn anaaagaana tctntggggg cttntntntt tatatcctct
W--> 293 540cntattgtnc tttcnntan cntctntcen ngannctcat tcccganacc ctctnnnnnc
W--> 294 600cgccttnenc tctentatan tttctnagtt gaaccgctcn tcccnctnca ctnttattnn
W--> 295 660ntnngcgggn cgcncncttt gtccctcntt aaccctgggg ntngcgagen tacnggctcn
W--> 296 720ctccctaata ctctgggcgg tnnngggcg nacgtcctcg ccttcgttcn naaatnnttc
W--> 297 780ntaantcca acntcngcn gcccgcctcc ggnnnnnnca atntntctc cccctattc
W--> 298 840tngctacna gcngtgatn atccctttct cannagcctn ttcnggggat aacngngnag
W--> 299 900ngannctctc tctttagtnc cnaancna tctctnctcc tcttctcng gtcgcgctnc
W--> 300 960tanancnctg gtcagttnnn tctctnatgn nncnnaggnt cccnntnct cncctcttc
W--> 301 1020ttgnnnactc ccngntgtc cnggantgn tcttcgcct cgganancnt gctcctntnt
W--> 302 1080tcncnanncg aanantctc ttnctaacac ncttcgcen aanacntttt nactctnccc
W--> 303 1140tcntccttcn ctnnctcgtc tnattntnan ttnctnctc annngtgac tcgttagenc
E--> 304 1200tccgntcttt ccnanccttc gcccctctt ccnctctcna nctatccc 1249
306 <210> SEQ ID NO: 12
307 <211> LENGTH: 373
308 <212> TYPE: DNA
309 <213> ORGANISM: Psuedomonas fluorescens
311 <220> FEATURE:
312 <221> NAME/KEY: variation
313 <222> LOCATION: (1)...(373)
314 <223> OTHER INFORMATION: n is a, t, c, or g.
316 <400> SEQUENCE: 12
E--> 317 tnattgtgta taagntcagg actagagntc ctctcttagt nacggttcgc agcgttttgc
W--> 318 60accgcacgt ccantgcgn cccaccccg tactagtga cagtggaana aactcgcccg
W--> 319 120gagtcgacnc gtgggtanta gtgaagcgt ggngangnt cncgntatna ggcntaanan
W--> 320 180ctgcatcacg aaagcngggg gaaggttctc naaaanttcn ccnatgaggg agaacacgga
W--> 321 240aancccttta ccnaggggc ggccngaaa tctggcaacn gancggmngg agaatcncc
W--> 322 300atttcgtcag tccatgggc accaccggga acatcatggg cgtcnntnc cngtactant
E--> 323 360cgaccgtggc caa 373
325 <210> SEQ ID NO: 13
326 <211> LENGTH: 683
327 <212> TYPE: DNA
328 <213> ORGANISM: Psuedomonas fluorescens
330 <220> FEATURE:

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331 <221> NAME/KEY: variation
332 <222> LOCATION: (1)...(683)
333 <223> OTHER INFORMATION: n is a, t, c, or g.
335 <400> SEQUENCE: 13
E--> 336 tgactgtgtg ttataagntc agnccgacnt ggnagtcnc ntntgggttg tangatccgc
W--> 337 60ancnattaag ctggccnngg gaaantcngg ttcaaccnng tgcnngcaat ganncnntat
W--> 338 120ttcactcncc cggcgtncac nccnngtan tantcgaccc ntggncanta ntantctaca
W--> 339 180nntgggtcaaaa acnttttcgan nnnntagng ngccctntn tanangtnan cttegtnacg
W--> 340 240ggggagggaaa angtccccg gnggccannn gccgagccta aaaaangagg cangtanggg
W--> 341 300tgngaaaaaa naatanctng atangaacnc acccnntttg acgccaatta accgangtac
W--> 342 360angaccnngn cnaactcatt tttagtgtn gcgacagaaa ttttnanggn cgcncangn
W--> 343 420gaanggtct cnaanggttn gnaaannnaa acnaggccct ccnntaatg gtggacccgc
W--> 344 480gggnaanntt nncncgant ggggttttga aattactttt caacaatctt caaaacntcc
W--> 345 540gggtcnancc agggagggnc aaaaaaaaaa tntttccgn gtngccnnaa aaatatccna
W--> 346 600aattttntcn ccccccccc nccnnaaaag aaggnggggg gggaagggga aaaagggggg
E--> 347 660aangaggggg gggaaggggg ggg
349 <210> SEQ ID NO: 14
350 <211> LENGTH: 672
351 <212> TYPE: DNA
352 <213> ORGANISM: Psuedomonas fluorescens
354 <220> FEATURE:
355 <221> NAME/KEY: variation
356 <222> LOCATION: (1)...(672)
357 <223> OTHER INFORMATION: n is a, t, c, or g.
359 <400> SEQUENCE: 14
E--> 360 gtgcttgtgt ataagntcag nccctggcct gngcgnac aactccggtt nccgtctaca
W--> 361 60nttttagcnaa ggatcggtca ttgctngtc tntggntan actnccggga cnatccacct
W--> 362 120caatactccn nccattnacg tctatggtaa ccnggaggtc ggtcancagn ncnattaccg
W--> 363 180gtinctaccng tggaaacttc gaaaatctng tggcnaacac gggacctgcy gtccccncca
W--> 364 240nttccgattc ngngganacn ncatggntgt cncnnacngg nngcnacncc attcctgnan
W--> 365 300gggngccaan ttcctttcnc ntcaanccgt nggnaacggg cccnaatncc gtnaacgtta
W--> 366 360ccnnnganaa atggctngtt ttccatcccc ccgggggman aaaccgggac ngaagatttc
W--> 367 420aanacccgcg cntntnattt taccnngggg nngcggggtc gnccccncn nnacnngtga
W--> 368 480naangggggg ctnttcaaan ttctntngtg tnanacnac cctgggggtt natantantt
W--> 369 540ncanaattnc gggnggaana ccaccggggc ttnannnctt nnaacnggnc nnncnaccnn
W--> 370 600ctttccnnnn ngggggggng ttccnncncc ccccenttnn nttnttttn aaanntttt
E--> 371 660gggggaaaaa aa
373 <210> SEQ ID NO: 15
374 <211> LENGTH: 1676
375 <212> TYPE: DNA
376 <213> ORGANISM: Psuedomonas fluorescens
378 <220> FEATURE:
379 <221> NAME/KEY: variation
380 <222> LOCATION: (1)...(1676)
381 <223> OTHER INFORMATION: n is a, t, c, or g.
383 <400> SEQUENCE: 15
E--> 384 tgcttgtgta taagatcagg gcccngcgcc nccnnantta ngctcgggtc aacgacacnn
W--> 385 60catnggtgcn gtggnanctc antttacnag gcncctaaaa ngcatnattg ttatncagtn
W--> 386 120ngncgaggtt gntcctccn tancggaagn natntgnnaa ctggaanga tttananttt

```

683

672

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W--> 387 180ttccantcgg tngntaccag nngtgantcn tcantttctg acaccenctg gtnncnntcc
W--> 388 240tgttcacncc tanannngac cncctctctcc gntgngggcc tggngcntaa tatnntaccg
W--> 389 300gcttttnant gctgtcagta tnanctctcn nagecgnaaa ntcnctctnc annccggtgn
W--> 390 360tntngtctcn cncctctctc nctcntacac tcactnactn tntnctgnna atcnntctnn
W--> 391 420ctgtantatc acggnacancn cgttctntgt ggggctcnct tganaggctc cccctnacct
W--> 392 480ctctannnac nggtctgggt atnnncctat aanagtcttg tgcattgtntc acagtnacat
W--> 393 540cgtcgccnnn cncgngtagc tctgcatent cgcccttttn tttctnttct ctengcaaan
W--> 394 600atcttntntn ctctcnntcn atcattattc ncangcgngg ggggtctcct cccctcnnn
W--> 395 660nctcngttc nanacangtc ntnttttagct atgtcttatg tncnctntc anttttctn
W--> 396 720cnccttcncc ncttcagann ggctnngnct gacctctata gtcgntctc tctctctct
W--> 397 780nctnntctct cngcnataac gcnctnctc ttctggctc tcnngctctc tntntntata
W--> 398 840tccnncgccc nttctctcta tctctcggnt ntgtgtctnt caattgtncn ctctctctgn
W--> 399 900cnnctgtcnn ntctancgtt ttcttgactt nannaatacn taccctctctt ngcctctctn
W--> 400 960cntntnctct cncgcctct ctngaccgc tncctctgcn cngcgcnatc tcttcttnc
W--> 401 1020gttctcnnnt tctcgcgnt ctctnngtac tngcttttcc cncctacctn ctcttgcctc
W--> 402 1080ttcctcgent cntctnctc tctcttctct ntctangtcn ncnccgncat nggctttctc
W--> 403 1140tcgctnctn tcnctcttct ntctntnccg tctcgtctng atcnntctct catcatntc
W--> 404 1200tntntntca tcanctntn tgnactctc cnatctgtnt ctctntctta ntntctctc
W--> 405 1260cttctnttc tcttanctcn cgtnnatnnc nttctctgat nctctnagt atntctatgt
W--> 406 1320acgctnnct tnatcgngnn cctntctcta tcanatcat nctagctnnc tctctatngt
W--> 407 1380cctgctctca ctntttctgc cnanatatnn atcnctnctc tnatctctcn tanattntn
W--> 408 1440cctntnaatg tttanaaatg ctctactcna nctctctntn tctnnnctc cagntcactc
W--> 409 1500tctananntg cctnncgtta taagntcttn tncgctttan tgcgtntnct atcantnccg
W--> 410 1560ctcttttntt ctctctcnc cntgtntctn ncacactntc ttcctctctt ctcnatatn
E--> 411 1620natgtcnnct tatnccnct tctatgctnt cncctntcna nccacantnt nntctc

```

1676

```

413 <210> SEQ ID NO: 16
414 <211> LENGTH: 721
415 <212> TYPE: DNA
416 <213> ORGANISM: Psuedomonas fluorescens
418 <220> FEATURE:
419 <221> NAME/KEY: variation
420 <222> LOCATION: (1)...(721)
421 <223> OTHER INFORMATION: n is a, t, c, or g.
423 <400> SEQUENCE: 16

```

```

E--> 424 tncctgtgta taagatcagg cctatngccg nctgnggntt ntctgggtgc ncgacgcgcc
W--> 425 60attcgaaaaa ancagctccg nnaccngttc caantacacn nngttgtncn nccgnagttc
W--> 426 120cagcttcngc ctgcgcacg tnnacaattc ctncnaaacc ctgggtgtgn tnttcnnaa
W--> 427 180gctnatgtan ganngtcnat nggncgtgnn gnactgtct accnagnctc angtnngcac
W--> 428 240caaccngagc ntcattcncg cnaacnccga acccngngg nctcgtctct ntcnaacnc
W--> 429 300cnncaantcc aacnccatng gttgtgtgcn cnacgacnng ngcgaaaacn ncgcnacnn
W--> 430 360ngncnagtc aagttccgc atacccacg cnggtcnggg ggtntcncct cctntctgt
W--> 431 420tccaaacatn nccatanaan nnnnggtntg ctgggggaat ccaancctc nctgnggtt
W--> 432 480cgatcnaaac aanatanggg tcaangnncn gccacttgcn tnatnaattt cncagtgcc
W--> 433 540cntnncnctn tgatnngcna agcnnncnnn ggggtgngg gggnnnttnc cennntatna
W--> 434 600antanaaacg gcngntcct tnnccnccan ggggtgntgn ngnttttnaa aacnctttt
E--> 435 660nnnnaaanan ccccccncct ntttncnng gannannatc cnnaannnn gttccnccc
E--> 436 721

```

720c

```

438 <210> SEQ ID NO: 17
439 <211> LENGTH: 452

```

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440 <212> TYPE: DNA
441 <213> ORGANISM: Psuedomonas fluorescens
443 <220> FEATURE:
444 <221> NAME/KEY: variation
445 <222> LOCATION: (1)...(452)
446 <223> OTHER INFORMATION: n is a, t, c, or g.
448 <400> SEQUENCE: 17
E--> 449 atnnngnnnn tncctgtgta taagntcagg gncncnctn tcnnaacttn gtctgggtcg
W--> 450 60ngctacacnn cannggnnac tggcagctcg gtnaccgcta cctnanaacg cttcantgtt
W--> 451 120cctcagcngg tccacgtcca gccttgagcc acatgtnaaa annngccna caancnngg
W--> 452 180ngtnaanntc caggnntgc ncgacgantg ccaatnnaan nttctnacb gtttcacctg
W--> 453 240gaangacctt gccganaccn anacnntcac caanggtgaa nncaactccc ggnagatnccg
W--> 454 300ctncacnccn gaccccaacg aatcctnccg cgnnggtttt nttagcanca tcgncgncan
W--> 455 360caaccangnc canttcccc cgntntcatt ccnccnanc gacggnnnnt ctgggcgtcn
E--> 456 420cccccccggt actantctac ncntnncaaa aa
458 <210> SEQ ID NO: 18
459 <211> LENGTH: 442
460 <212> TYPE: DNA
461 <213> ORGANISM: Psuedomonas fluorescens
463 <220> FEATURE:
464 <221> NAME/KEY: variation
465 <222> LOCATION: (1)...(422)
466 <223> OTHER INFORMATION: n is a, t, c, or g.
468 <400> SEQUENCE: 18
E--> 469 tncctgtgta taagntcagg ntctnagatg agctcggtag ttcangagnt tttctgcgac
W--> 470 60cgcgnnnccg acgntgnaa tcgntggcna ggtngcnta nacannnaa agtanncccc
W--> 471 120tcgaancgnt cnntgacctc ctgntccaaa tngtcacng cattggncga cgcngcnca
W--> 472 180cccncaactt cgtctgaent cccaaaancn gcctgggcn ngcncgncng gattngccc
W--> 473 240gacatcnct nancaaantr cccnccgcn tactngncca nccttgacca nttttgcnc
W--> 474 300tctntcctt actgggtcng cttegnctcc ggnntgctna ccannatggt ccnaancctg
W--> 475 360ctgtcctnca ctctcaaatn cgccccggc caacntgct gatcgnttc nncnccnag
E--> 476 420tctattcaa cccctgcccc aa
478 <210> SEQ ID NO: 19
479 <211> LENGTH: 538
480 <212> TYPE: DNA
481 <213> ORGANISM: Psuedomonas fluorescens
483 <220> FEATURE:
484 <221> NAME/KEY: variation
485 <222> LOCATION: (1)...(538)
486 <223> OTHER INFORMATION: n is a, t, c, or g.
488 <400> SEQUENCE: 19
E--> 489 ctttgttgta taagnatcag aactagagc ttgccccttc tncancnctt cnatggacag
W--> 490 60cggttttcgg gcgctgagc aacgatctgt ccacagttna ncaccannag gcgntccacc
W--> 491 120atcaanagaa aggannccg gtnctnacc acnnacacan gtcttggtat cnaccacggc
W--> 492 180agccaagcgn tgtttcaaac gttcttcagc ngtgtgtgct atggatctgg ttggttcgtc
W--> 493 240caanaacaag ataggcgtgt tnancncnt ncnactngac acgtggaaat tntngctcta
W--> 494 300accncccgac angttctgtc nncnctncc naatnnnaat tcataacctt ncngatgcn
W--> 495 360gcggggcaaat tcatncncc cgccanttc acggnctgga acacanttca actncnagct
W--> 496 420ttcnggcgcc naaaantctt gttgtcnccc aggnntttnn nancnccng atnttttgg

```

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E--> 497 480ggnncccttnc cnaantttntt nnnccnctcc cntnannttg aanntngnng gatgttna 538

499 <210> SEQ ID NO: 20

500 <211> LENGTH: 218

501 <212> TYPE: DNA

502 <213> ORGANISM: Psuedomonas fluorescens

504 <220> FEATURE:

505 <221> NAME/KEY: variation

506 <222> LOCATION: (1)...(218)

507 <223> OTHER INFORMATION: n is a, t, c, or g.

509 <400> SEQUENCE: 20

E--> 510 tnatttggtg ataagttcag gttgctngnt gnaagccatc cggccaagg gttgccggcg

W--> 511 60tcaccacat ngtagtagtc nncgcgtggc cnaaacgggtg angctcncat attgatgctt

W--> 512 120gccaacgntt naaaaaaag tatngacagg gtnttaacca tcagnttntn ccnaangta

E--> 513 180ctagtctacc cgtggccana naantnnann nntggnca

686 <210> SEQ ID NO: 34

687 <211> LENGTH: 595

688 <212> TYPE: PRT

689 <213> ORGANISM: Escherichia coli

691 <400> SEQUENCE: 34

692 Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Ile Thr Gln Asn 1

E--> 693 5 10 15 Asn Ile Asn Lys Asn Gln Ser Ala

694 Leu Ser Ser Ser Ile Glu Arg Leu 20 25

E--> 695 30 Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln

E--> 696 35 40 45 Ala Ile Ala Asn Arg Phe

697 Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala 50 55

E--> 698 60 Ala Arg Asn Ala Asn Asp Gly Ile Ser Val Ala Gln Thr Thr Glu

E--> 699 Gly65 70 75 80 Ala Leu Ser

700 Glu Ile Asn Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr 85

E--> 701 90 95 Val Gln Ala Ser Thr Gly Thr Asn Ser Asp Ser Asp Leu

E--> 702 Asp Ser Ile 100 105 110 Gln

703 Asp Glu Ile Lys Ser Arg Leu Asp Glu Ile Asp Arg Val Ser Gly 115

E--> 704 120 125 Gln Thr Gln Phe Asn Gly Val Asn Val Leu Ala

705 Lys Asp Gly Ser Met 130 135 140

706 Lys Ile Gln Val Gly Ala Asn Asp Gly Gln Thr Ile Thr Ile Asp Leu145

E--> 707 150 155 160Lys Lys Ile Asp Ser Asp Thr Leu Gly

708 Leu Asn Gly Phe Asn Val Asn 165 170

E--> 709 175 Gly Ser Gly Thr Ile Ala Asn Lys Ala Ala Thr Ile Ser Asp Leu Thr

E--> 710 180 185 190 Ala Ala Lys Met Asp Ala Ala

711 Thr Asn Thr Ile Thr Thr Thr Asn Asn 195 200

E--> 712 205 Ala Leu Thr Ala Ser Lys Ala Leu Asp Gln Leu Lys Asp Gly Asp Thr

E--> 713 210 215 220 Val Thr Ile Lys Ala

714 Asp Ala Ala Gln Thr Ala Thr Val Tyr Thr Tyr225 230

E--> 715 235 240Asn Ala Ser Ala Gly Asn Phe Ser Phe Ser Asn Val Ser Asn

E--> 716 Asn Thr 245 250 255 Ser Ala

717 Lys Ala Gly Asp Val Ala Ala Ser Leu Leu Pro Pro Ala Gly 260

E--> 718 265 270 Gln Thr Ala Ser Gly Val Tyr Lys Ala Ala Ser Gly

719 Glu Val Asn Phe 275 280 285

720 Asp Val Asp Ala Asn Gly Lys Ile Thr Ile Gly Gly Gln Glu Ala Tyr 290

E--> 721 295 300 Leu Thr Ser Asp Gly Asn Leu Thr Thr Asn

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

major formatting error

see 37 (FR 1,822 (d) (1)-(5) and Sample provided at back

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722 Asp Ala Gly Gly Ala Thr305          310          315
E--> 723 320Ala Ala Thr Leu Asp Gly Leu Phe Lys Lys Ala Gly Asp Gly Gln Ser
E--> 724 325          330          335 Ile Gly Phe Asn Lys Thr Ala Ser
725 Val Thr Met Gly Gly Thr Thr Tyr          340          345
E--> 726 350          Asn Phe Lys Thr Gly Ala Asp Ala Gly Ala Ala Thr Ala Asn Ala Gly
E--> 727 355          360          365          Val Ser Phe Thr Asp Thr
728 Ala Ser Lys Glu Thr Val Leu Asn Lys Val          370          375
E--> 729 380          Ala Thr Ala Lys Gln Gly Thr Ala Val Ala Ala Asn Gly Asp Thr
E--> 730 Ser385          390          395          400Ala Thr Ile
731 Thr Tyr Lys Ser Gly Val Gln Thr Tyr Gln Ala Val Phe          405
E--> 732 410          415 Ala Ala Gly Asp Gly Thr Ala Ser Ala Lys Tyr Ala Asp
E--> 733 Asn Thr Asp          420          425          430          Val
734 Ser Asn Ala Thr Ala Thr Tyr Thr Asp Ala Asp Gly Glu Met Thr          435
E--> 735 440          445          Thr Ile Gly Ser Tyr Thr Thr Lys Tyr Ser Ile
736 Asp Ala Asn Asn Gly          450          455          460
737 Lys Val Thr Val Asp Ser Gly Thr Gly Ser Gly Lys Tyr Ala Pro Lys465
E--> 738 470          475          480Val Gly Ala Glu Val Tyr Val Ser Ala
739 Asn Gly Thr Leu Thr Thr Asp          485          490
E--> 740 495 Ala Thr Ser Glu Gly Thr Val Thr Lys Asp Pro Leu Lys Ala Leu Asp
E--> 741 500          505          510          Glu Ala Ile Ser Ser Ile Asp
742 Lys Phe Arg Ser Ser Leu Gly Ala Ile          515          520
E--> 743 525          Gln Asn Arg Leu Asp Ser Ala Val Thr Asn Leu Asn Asn Thr Thr Thr
E--> 744 530          535          540          Asn Leu Ser Glu Ala
745 Gln Ser Arg Ile Gln Asp Ala Asp Tyr Ala Thr545          550
E--> 746 555          560Glu Val Ser Asn Met Ser Lys Ala Gln Ile Ile Gln Gln Ala
E--> 747 Gly Asn          565          570          575          Ser Val
748 Leu Ala Lys Ala Asn Gln Val Pro Gln Gln Val Leu Ser Leu          580
E--> 749 585          590          Leu Gln Gly          595
751 <210> SEQ ID NO: 35
752 <211> LENGTH: 119
753 <212> TYPE: PRT
754 <213> ORGANISM: Escherichia coli
756 <400> SEQUENCE: 35
757 Met Gly Ile Met His Thr Ser Glu Leu Leu Lys His Ile Tyr Asp Ile 1
E--> 758 5          10          15          Asn Leu Ser Tyr Leu Leu Leu Ala
759 Gln Arg Leu Ile Val Gln Asp Lys          20          25
E--> 760 30 Ala Ser Ala Met Phe Arg Leu Gly Ile Asn Glu Glu Met Ala Thr Thr
E--> 761 35          40          45          Leu Ala Ala Leu Thr Leu
762 Pro Gln Met Val Lys Leu Ala Glu Thr Asn          50          55
E--> 763 60          Gln Leu Val Cys His Phe Arg Phe Asp Ser His Gln Thr Ile Thr
E--> 764 Gln65          70          75          80 Leu Thr Gln
765 Asp Ser Arg Val Asp Asp Leu Gln Gln Ile His Thr Gly          85
E--> 766 90          95          Ile Met Leu Ser Thr Arg Leu Leu Asn Asp Val Asn Gln
E--> 767 Pro Glu Glu          100          105          110          Ala
E--> 768 Leu Arg Lys Lys Arg Ala          115
770 <210> SEQ ID NO: 36
771 <211> LENGTH: 295
772 <212> TYPE: PRT
773 <213> ORGANISM: Escherichia coli

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775 <400> SEQUENCE: 36

776 Met Leu Ile Leu Leu Gly Tyr Leu Val Val Leu Gly Thr Val Phe Gly 1

E--> 777 5 10 15 Gly Tyr Leu Met Thr Gly Gly Ser

778 Leu Gly Ala Leu Tyr Gln Pro Ala 20 25

E--> 779 30 Glu Leu Val Ile Ile Ala Gly Ala Gly Ile Gly Ser Phe Ile Val Gly

E--> 780 35 40 45 Asn Asn Gly Lys Ala Ile

781 Lys Gly Thr Leu Lys Ala Leu Pro Leu Leu 50 55

E--> 782 60 Phe Arg Arg Ser Lys Tyr Thr Lys Ala Met Tyr Met Asp Leu Leu

E--> 783 Ala65 70 75 80 Leu Leu Tyr

784 Arg Leu Met Ala Lys Ser Arg Gln Met Gly Met Phe Ser 85

E--> 785 90 95 Leu Glu Arg Asp Ile Glu Asn Pro Arg Glu Ser Glu Ile

E--> 786 Phe Ala Ser 100 105 110 Tyr

787 Pro Arg Ile Leu Ala Asp Ser Val Met Leu Asp Phe Ile Val Asp 115

E--> 788 120 125 Tyr Leu Arg Leu Ile Ile Ser Gly His Met Asn

789 Thr Phe Glu Ile Glu 130 135 140

790 Ala Leu Met Asp Glu Glu Ile Glu Thr His Glu Ser Glu Ala Glu Val 145

E--> 791 150 155 160 Pro Ala Asn Ser Leu Ala Leu Val Gly

792 Asp Ser Leu Pro Ala Phe Gly 165 170

E--> 793 175 Ile Val Ala Ala Val Met Gly Val Val His Ala Leu Gly Ser Ala Asp

E--> 794 180 185 190 Arg Pro Ala Ala Glu Leu Gly

795 Ala Leu Ile Ala His Ala Met Val Gly 195 200

E--> 796 205 Thr Phe Leu Gly Ile Leu Leu Ala Tyr Gly Phe Ile Ser Pro Leu Ala

E--> 797 210 215 220 Thr Val Leu Arg Gln

798 Lys Ser Ala Glu Thr Ser Lys Met Met Gln Cys 225 230

E--> 799 235 240 Val Lys Val Thr Leu Leu Ser Asn Leu Asn Gly Tyr Ala Pro

E--> 800 Pro Ile 245 250 255 Ala Val

801 Glu Phe Gly Arg Lys Thr Leu Tyr Ser Ser Glu Arg Pro Ser 260

E--> 802 265 270 Phe Ile Glu Leu Glu Glu His Val Arg Ala Val Lys

803 Asn Pro Gln Gln 275 280 285

E--> 804 Gln Thr Thr Thr Glu Glu Ala 290 295

806 <210> SEQ ID NO: 37

807 <211> LENGTH: 308

808 <212> TYPE: PRT

809 <213> ORGANISM: Escherichia coli

811 <400> SEQUENCE: 37

812 Met Lys Asn Gln Ala His Pro Ile Ile Val Val Lys Arg Arg Lys Ala 1

E--> 813 5 10 15 Lys Ser His Gly Ala Ala His Gly

814 Ser Trp Lys Ile Ala Tyr Ala Asp 20 25

E--> 815 30 Phe Met Thr Ala Met Met Ala Phe Phe Leu Val Met Trp Leu Ile Ser

E--> 816 35 40 45 Ile Ser Ser Pro Lys Glu

817 Leu Ile Gln Ile Ala Glu Tyr Phe Arg Thr 50 55

E--> 818 60 Pro Leu Ala Thr Ala Val Thr Gly Gly Asp Arg Ile Ser Asn Ser

E--> 819 Glu65 70 75 80 Ser Pro Ile

820 Pro Gly Gly Gly Asp Asp Tyr Thr Gln Ser Gln Gly Glu 85

E--> 821 90 95 Val Asn Lys Gln Pro Asn Ile Glu Glu Leu Lys Lys Arg

E--> 822 Met Glu Gln 100 105 110 Ser

823 Arg Leu Arg Lys Leu Arg Gly Asp Leu Asp Gln Leu Ile Glu Ser 115

E--> 824 120 125 Asp Pro Lys Leu Arg Ala Leu Arg Pro His Leu

825 Lys Ile Asp Leu Val 130 135 140

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```

      826 Gln Glu Gly Leu Arg Ile Gln Ile Ile Asp Ser Gln Asn Arg Pro Met145
E--> 827 150          155          160Phe Arg Thr Gly Ser Ala Asp Val Glu
      828 Pro Tyr Met Arg Asp Ile Leu          165          170
E--> 829 175      Arg Ala Ile Ala Pro Val Leu Asn Gly Ile Pro Asn Arg Ile Ser Leu
E--> 830 180          185          190          Ser Gly His Thr Asp Asp Phe
      831 Pro Tyr Ala Ser Gly Glu Lys Gly Tyr          195          200
E--> 832 205          Ser Asn Trp Glu Leu Ser Ala Asp Arg Ala Asn Ala Ser Arg Arg Glu
E--> 833 210          215          220          Leu Met Val Gly Gly
      834 Leu Asp Ser Gly Lys Val Leu Arg Val Val Gly225          230
E--> 835 235          240Met Ala Ala Thr Met Arg Leu Ser Asp Arg Gly Pro Asp Asp
E--> 836 Ala Val          245          250          255      Asn Arg
      837 Arg Ile Ser Leu Leu Val Leu Asn Lys Gln Ala Glu Gln Ala          260
E--> 838 265          270          Ile Leu His Glu Asn Ala Glu Ser Gln Asn Glu Pro
      839 Val Ser Ala Leu          275          280          285
      840 Glu Lys Pro Glu Val Ala Pro Gln Val Ser Val Pro Thr Met Pro Ser          290
E--> 841 295          300          Ala Glu Pro Arg305
      843 <210> SEQ ID NO: 38
      844 <211> LENGTH: 245
      845 <212> TYPE: PRT
      846 <213> ORGANISM: Escherichia coli
      848 <400> SEQUENCE: 38
      849 Met Arg Arg Leu Leu Ser Val Ala Pro Val Leu Leu Trp Leu Ile Thr 1
E--> 850 5          10          15      Pro Leu Ala Phe Ala Gln Leu Pro
      851 Gly Ile Thr Ser Gln Pro Leu Pro          20          25
E--> 852 30      Gly Gly Gly Gln Ser Trp Ser Leu Pro Val Gln Thr Leu Val Phe Ile
E--> 853 35          40          45          Thr Ser Leu Thr Phe Ile
      854 Pro Ala Ile Leu Leu Met Met Thr Ser Phe          50          55
E--> 855 60          Thr Arg Ile Ile Ile Val Phe Gly Leu Leu Arg Asn Ala Leu Gly
E--> 856 Thr65          70          75          80 Pro Ser Ala
      857 Pro Pro Asn Gln Val Leu Leu Gly Leu Ala Leu Phe Leu          85
E--> 858 90          95      Thr Phe Phe Ile Met Ser Pro Val Ile Asp Lys Ile Tyr
E--> 859 Val Asp Ala          100          105          110      Tyr
      860 Gln Pro Phe Ser Glu Glu Lys Ile Ser Met Gln Glu Ala Leu Glu          115
E--> 861 120          125          Lys Gly Ala Gln Pro Leu Arg Glu Phe Met Leu
      862 Arg Gln Thr Arg Glu          130          135          140
      863 Ala Asp Leu Gly Leu Phe Ala Arg Leu Ala Asn Thr Gly Pro Leu Gln145
E--> 864 150          155          160Gly Pro Glu Ala Val Pro Met Arg Ile
      865 Leu Leu Pro Ala Tyr Val Thr          165          170
E--> 866 175      Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Thr Ile Phe Ile Pro
E--> 867 180          185          190          Phe Leu Ile Ile Asp Leu Val
      868 Ile Ala Ser Val Leu Met Ala Leu Gly          195          200
E--> 869 205          Met Met Met Val Pro Pro Ala Thr Ile Ala Leu Pro Phe Lys Leu Met
E--> 870 210          215          220          Leu Phe Val Leu Val
      871 Asp Gly Trp Gln Leu Leu Val Gly Ser Leu Ala225          230
E--> 872 235          240Gln Ser Phe Tyr Ser          245
      874 <210> SEQ ID NO: 39
      875 <211> LENGTH: 375
      876 <212> TYPE: PRT
      877 <213> ORGANISM: Escherichia coli

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879 <400> SEQUENCE: 39
880 Met Ile Arg Leu Ala Pro Leu Ile Thr Ala Asp Val Asp Thr Thr Thr 1
E--> 881 5          10          15          Leu Pro Gly Gly Lys Ala Ser Asp
882 Ala Ala Gln Asp Phe Leu Ala Leu          20          25
E--> 883 30          Leu Ser Glu Ala Leu Ala Gly Glu Thr Thr Thr Asp Lys Ala Ala Pro
E--> 884 35          40          45          Gln Leu Leu Val Ala Thr
885 Asp Lys Pro Thr Thr Lys Gly Glu Pro Leu          50          55
E--> 886 60          Ile Ser Asp Ile Val Ser Asp Ala Gln Gln Ala Asn Leu Leu Ile
E--> 887 Pro65          70          75          80 Val Asp Glu
888 Thr Pro Pro Val Ile Asn Asp Glu Gln Ser Thr Ser Thr          85
E--> 889 90          95          Pro Leu Thr Thr Ala Gln Thr Met Ala Leu Ala Ala Val
E--> 890 Ala Asp Lys          100          105          110          Asn
891 Thr Thr Lys Asp Glu Lys Ala Asp Asp Leu Asn Glu Asp Val Thr          115
E--> 892 120          125          Ala Ser Leu Ser Ala Leu Phe Ala Met Leu Pro
893 Gly Phe Asp Asn Thr          130          135          140
894 Pro Lys Val Thr Asp Ala Pro Ser Thr Val Leu Pro Thr Glu Lys Pro145
E--> 895 150          155          160Thr Leu Phe Thr Lys Leu Thr Ser Glu
896 Gln Leu Thr Thr Ala Gln Pro          165          170
E--> 897 175          Asp Asp Ala Pro Gly Thr Pro Ala Gln Pro Leu Thr Pro Leu Val Ala
E--> 898 180          185          190          Glu Ala Gln Ser Lys Ala Glu
899 Val Ile Ser Thr Pro Ser Pro Val Thr          195          200
E--> 900 205          Ala Ala Ala Ser Pro Leu Ile Thr Pro His Gln Thr Gln Pro Leu Pro
E--> 901 210          215          220          Thr Val Ala Ala Pro
902 Val Leu Ser Ala Pro Leu Gly Ser His Glu Trp225          230
E--> 903 235          240Gln Gln Ser Leu Ser Gln His Ile Ser Leu Phe Thr Arg Gln
E--> 904 Gly Gln          245          250          255          Gln Ser
905 Ala Glu Leu Arg Leu His Pro Gln Asp Leu Gly Glu Val Gln          260
E--> 906 265          270          Ile Ser Leu Lys Val Asp Asp Asn Gln Ala Gln Ile
907 Gln Met Val Ser          275          280          285
908 Pro His Gln His Val Arg Ala Ala Leu Glu Ala Ala Leu Pro Val Leu          290
E--> 909 295          300          Arg Thr Gln Leu Ala Glu Ser Gly Ile Gln
910 Leu Gly Gln Ser Asn Ile305          310          315
E--> 911 320Ser Gly Glu Ser Phe Ser Gly Gln Gln Gln Ala Ala Ser Gln Gln Gln
E--> 912 325          330          335          Gln Ser Gln Arg Thr Ala Asn His
913 Glu Pro Leu Ala Gly Glu Asp Asp          340          345
E--> 914 350          Asp Thr Leu Pro Val Pro Val Ser Leu Gln Gly Arg Val Thr Gly Asn
E--> 915 355          360          365          Ser Gly Val Asp Ile Phe
E--> 916 Ala          370          375
918 <210> SEQ ID NO: 40
919 <211> LENGTH: 547
920 <212> TYPE: PRT
921 <213> ORGANISM: Escherichia coli
923 <400> SEQUENCE: 40
924 Met Ser Ser Leu Ile Asn Asn Ala Met Ser Gly Leu Asn Ala Ala Gln 1
E--> 925 5          10          15          Ala Ala Leu Asn Thr Ala Ser Asn
926 Asn Ile Ser Ser Tyr Asn Val Ala          20          25
E--> 927 30          Gly Tyr Thr Arg Gln Thr Thr Ile Met Ala Gln Ala Asn Ser Thr Leu
E--> 928 35          40          45          Gly Ala Gly Gly Trp Val
929 Gly Asn Gly Val Tyr Val Ser Gly Val Gln          50          55

```

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E--> 930 60          Arg Glu Tyr Asp Ala Phe Ile Thr Asn Gln Leu Arg Ala Ala Gln
E--> 931 Thr65          70          75          80 Gln Ser Ser
      932 Gly Leu Thr Ala Arg Tyr Glu Gln Met Ser Lys Ile Asp          85
E--> 933 90          95          Asn Met Leu Ser Thr Ser Thr Ser Ser Leu Ala Thr Gln
E--> 934 Met Gln Asp          100          105          110          Phe
      935 Phe Thr Ser Leu Gln Thr Leu Val Ser Asn Ala Glu Asp Pro Ala          115
E--> 936 120          125          Ala Arg Gln Ala Leu Ile Gly Lys Ser Glu Gly
      937 Leu Val Asn Gln Phe          130          135          140
      938 Lys Thr Thr Asp Gln Tyr Leu Arg Asp Gln Asp Lys Gln Val Asn Ile145
E--> 939 150          155          160Ala Ile Gly Ala Ser Val Asp Gln Ile
      940 Asn Asn Tyr Ala Lys Gln Ile          165          170
E--> 941 175          Ala Ser Leu Asn Asp Gln Ile Ser Arg Leu Thr Gly Val Gly Ala Gly
E--> 942 180          185          190          Ala Ser Pro Asn Asn Leu Leu
      943 Asp Gln Arg Asp Gln Leu Val Ser Glu          195          200
E--> 944 205          Leu Asn Gln Ile Val Gly Val Glu Val Ser Val Gln Asp Gly Gly Thr
E--> 945 210          215          220          Tyr Asn Ile Thr Met
      946 Ala Asn Gly Tyr Ser Leu Val Gln Gly Ser Thr225          230
E--> 947 235          240Ala Arg Gln Leu Ala Ala Val Pro Ser Ser Ala Asp Pro Ser
E--> 948 Arg Thr          245          250          255          Thr Val
      949 Ala Tyr Val Asp Gly Thr Ala Gly Asn Ile Glu Ile Pro Glu          260
E--> 950 265          270          Lys Leu Leu Asn Thr Gly Ser Leu Gly Gly Ile Leu
      951 Thr Phe Arg Ser          275          280          285
      952 Gln Asp Leu Asp Gln Thr Arg Asn Thr Leu Gly Gln Leu Ala Leu Ala          290
E--> 953 295          300          Phe Ala Glu Ala Phe Asn Thr Gln His Lys
      954 Ala Gly Phe Asp Ala Asn305          310          315
E--> 955 320Gly Asp Ala Gly Glu Asp Phe Phe Ala Ile Gly Lys Pro Ala Val Leu
E--> 956 325          330          335          Gln Asn Thr Lys Asn Lys Gly Asp
      957 Val Ala Ile Gly Ala Thr Val Thr          340          345
E--> 958 350          Asp Ala Ser Ala Val Leu Ala Thr Asp Tyr Lys Ile Ser Phe Asp Asn
E--> 959 355          360          365          Asn Gln Trp Gln Val Thr
      960 Arg Leu Ala Ser Asn Thr Thr Phe Thr Val          370          375
E--> 961 380          Thr Pro Asp Ala Asn Gly Lys Val Ala Phe Asp Gly Leu Glu Leu
E--> 962 Thr385          390          395          400Phe Thr Gly
      963 Thr Pro Ala Val Asn Asp Ser Phe Thr Leu Lys Pro Val          405
E--> 964 410          415          Ser Asp Ala Ile Val Asn Met Asp Val Leu Ile Thr Asp
E--> 965 Glu Ala Lys          420          425          430          Ile
      966 Ala Met Ala Ser Glu Glu Asp Ala Gly Asp Ser Asp Asn Arg Asn          435
E--> 967 440          445          Gly Gln Ala Leu Leu Asp Leu Gln Ser Asn Ser
      968 Lys Thr Val Gly Gly          450          455          460
      969 Ala Lys Ser Phe Asn Asp Ala Tyr Ala Ser Leu Val Ser Asp Ile Gly465
E--> 970 470          475          480Asn Lys Thr Ala Thr Leu Lys Thr Ser
      971 Ser Ala Thr Gln Gly Asn Val          485          490
E--> 972 495          Val Thr Gln Leu Ser Asn Gln Gln Gln Ser Ile Ser Gly Val Asn Leu
E--> 973 500          505          510          Asp Glu Glu Tyr Gly Asn Leu
      974 Gln Arg Phe Gln Gln Tyr Tyr Leu Ala          515          520
E--> 975 525          Asn Ala Gln Val Leu Gln Thr Ala Asn Ala Ile Phe Asp Ala Leu Ile
E--> 976 530          535          540          Asn Ile Arg545
      978 <210> SEQ ID NO: 41
      979 <211> LENGTH: 566

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980 <212> TYPE: PRT
981 <213> ORGANISM: Psuedomonas aeruginosa
983 <400> SEQUENCE: 41
984 Met Asn Asp Ser Ile Gln Leu Ser Gly Leu Ser Arg Gln Leu Val Gln 1
E--> 985 5      10      15      Ala Asn Leu Leu Asp Glu Lys Thr
986 Ala Leu Gln Ala Gln Thr Gln Ala      20      25
E--> 987 30      Gln Arg Asn Lys Leu Ser Leu Val Thr His Leu Val Gln Asn Lys Leu
E--> 988 35      40      45      Val Ser Gly Leu Ala Leu
989 Ala Glu Leu Ser Ala Glu Gln Phe Gly Ile      50      55
E--> 990 60      Ala Tyr Cys Asp Leu Asn Ser Leu Asp Arg Glu Ser Phe Pro Arg
E--> 991 Asp65      70      75      80 Ala Ile Ser
992 Glu Lys Leu Val Arg Gln His Arg Val Ile Pro Leu Trp      85
E--> 993 90      95      Arg Arg Gly Asn Lys Leu Phe Val Gly Ile Ser Asp Ala
E--> 994 Ala Asn His      100      105      110      Gln
995 Ala Ile Asn Asp Val Gln Phe Ser Thr Gly Leu Thr Thr Glu Ala      115
E--> 996 120      125      Ile Leu Val Glu Asp Asp Lys Leu Gly Leu Ala
997 Ile Asp Lys Leu Phe      130      135      140
998 Glu Asn Ala Thr Asp Gly Leu Ala Gly Leu Asp Asp Val Asp Leu Glu145
E--> 999 150      155      160Gly Leu Asp Val Gly Val Lys Glu Thr
1000 Ser Gly Gln Glu Asp Thr Gly      165      170
E--> 1001 175      Ala Glu Ala Asp Asp Ala Pro Val Val Arg Phe Val Asn Lys Met Leu
E--> 1002 180      185      190      Leu Asp Ala Ile Lys Gly Gly
1003 Ser Ser Asp Leu His Phe Glu Pro Tyr      195      200
E--> 1004 205      Glu Lys Ile Tyr Arg Val Arg Phe Arg Thr Asp Gly Met Leu His Glu
E--> 1005 210      215      220      Val Ala Lys Pro Pro
1006 Ile Gln Leu Ala Ser Arg Ile Ser Ala Arg Leu225      230
E--> 1007 235      240Lys Val Met Ala Gly Leu Asp Ile Ser Glu Arg Arg Lys Pro
E--> 1008 Gln Asp      245      250      255      Gly Arg
1009 Ile Lys Met Arg Val Ser Lys Thr Lys Ser Ile Asp Phe Arg      260
E--> 1010 265      270      Val Asn Thr Leu Pro Thr Leu Trp Gly Glu Lys Ile
1011 Val Met Arg Ile      275      280      285
1012 Leu Asp Ser Ser Ser Ala Gln Met Gly Ile Asp Ala Leu Gly Tyr Glu      290
E--> 1013 295      300      Glu Asp Gln Lys Glu Leu Tyr Leu Ala Ala
1014 Leu Lys Gln Pro Gln Gly305      310      315
E--> 1015 320Met Ile Leu Val Thr Gly Pro Thr Gly Ser Gly Lys Thr Val Ser Leu
E--> 1016 325      330      335      Tyr Thr Gly Leu Asn Ile Leu Asn
1017 Thr Thr Asp Ile Asn Ile Ser Thr      340      345
E--> 1018 350      Ala Glu Asp Pro Val Glu Ile Asn Leu Glu Gly Ile Asn Gln Val Asn
E--> 1019 355      360      365      Val Asn Pro Arg Gln Gly
1020 Met Asp Phe Ser Gln Ala Leu Arg Ala Phe      370      375
E--> 1021 380      Leu Arg Gln Asp Pro Asp Val Ile Met Val Gly Glu Ile Arg Asp
E--> 1022 Leu385      390      395      400Glu Thr Ala
1023 Glu Ile Ala Ile Lys Ala Ala Gln Thr Gly His Met Val      405
E--> 1024 410      415      Met Ser Thr Leu His Thr Asn Ser Ala Ala Glu Thr Leu
E--> 1025 Thr Arg Leu      420      425      430      Leu
1026 Asn Met Gly Val Pro Ala Phe Asn Leu Ala Thr Ser Val Asn Leu      435
E--> 1027 440      445      Ile Ile Ala Gln Arg Leu Ala Arg Lys Leu Cys
1028 Ser His Cys Lys Lys      450      455      460
1029 Glu His Asp Val Pro Lys Glu Thr Leu Leu His Glu Gly Phe Pro Glu465

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```

E--> 1030 470          475          480Glu Leu Ile Gly Thr Phe Lys Leu Tyr
      1031 Ser Pro Val Gly Cys Asp His          485          490
E--> 1032 495      Cys Lys Asn Gly Tyr Lys Gly Arg Val Gly Ile Tyr Glu Val Val Lys
E--> 1033 500          505          510          Asn Thr Pro Ala Leu Gln Arg
      1034 Ile Ile Met Glu Glu Gly Asn Ser Ile          515          520
E--> 1035 525          Glu Ile Ala Glu Gln Ala Arg Lys Glu Gly Phe Asn Asp Leu Arg Thr
E--> 1036 530          535          540          Ser Gly Leu Leu Lys
      1037 Ala Met Gln Gly Ile Thr Ser Leu Glu Glu Val545          550
E--> 1038 555          560Asn Arg Val Thr Lys Asp          565
      1040 <210> SEQ ID NO: 42
      1041 <211> LENGTH: 406
      1042 <212> TYPE: PRT
      1043 <213> ORGANISM: Psuedomonas aeruginosa
      1045 <400> SEQUENCE: 42
      1046 Met Ala Asp Lys Ala Leu Lys Thr Ser Val Phe Ile Trp Glu Gly Thr 1
E--> 1047 5          10          15      Asp Lys Lys Gly Ala Lys Val Lys
      1048 Gly Glu Leu Thr Gly Gln Asn Pro          20          25
E--> 1049 30      Met Leu Val Lys Ala His Leu Arg Lys Gln Gly Ile Asn Pro Leu Lys
E--> 1050 35          40          45          Val Arg Lys Lys Gly Ile
      1051 Ser Leu Leu Gly Ala Gly Lys Lys Val Lys          50          55
E--> 1052 60          Pro Met Asp Ile Ala Leu Phe Thr Arg Gln Met Ala Thr Met Met
E--> 1053 Gly65          70          75          80 Ala Gly Val
      1054 Pro Leu Leu Gln Ser Phe Asp Ile Ile Gly Glu Gly Phe          85
E--> 1055 90          95      Asp Asn Pro Asn Met Arg Lys Leu Val Asp Glu Ile Lys
E--> 1056 Gln Glu Val          100          105          110      Ser
      1057 Ser Gly Asn Ser Leu Ala Asn Ser Leu Arg Lys Lys Pro Gln Tyr          115
E--> 1058 120          125          Phe Asp Glu Leu Tyr Cys Asn Leu Val Asp Ala
      1059 Gly Glu Gln Ser Gly          130          135          140
      1060 Ala Leu Glu Asn Leu Leu Asp Arg Val Ala Thr Tyr Lys Glu Lys Thr145
E--> 1061 150          155          160Glu Ser Leu Lys Ala Lys Ile Lys Lys
      1062 Ala Met Thr Tyr Pro Ile Ala          165          170
E--> 1063 175      Val Ile Ile Val Ala Leu Ile Val Ser Ala Ile Leu Leu Ile Lys Val
E--> 1064 180          185          190          Val Pro Gln Phe Gln Ser Val
      1065 Phe Glu Gly Phe Gly Ala Glu Leu Pro          195          200
E--> 1066 205          Ala Phe Thr Gln Met Ile Val Asn Leu Ser Glu Phe Met Gln Glu Trp
E--> 1067 210          215          220          Trp Phe Phe Ile Ile
      1068 Leu Ala Ile Ala Ile Phe Gly Phe Ala Phe Lys225          230
E--> 1069 235          240Glu Leu His Lys Arg Ser Gln Lys Phe Arg Asp Thr Leu Asp
E--> 1070 Arg Thr          245          250          255      Ile Leu
      1071 Lys Leu Pro Ile Phe Gly Gly Ile Val Tyr Lys Ser Ala Val          260
E--> 1072 265          270          Ala Arg Tyr Ala Arg Thr Leu Ser Thr Thr Phe Ala
      1073 Ala Gly Val Pro          275          280          285
      1074 Leu Val Asp Ala Leu Asp Ser Val Ser Gly Ala Thr Gly Asn Ile Val          290
E--> 1075 295          300          Phe Lys Asn Ala Val Ser Lys Ile Lys Gln
      1076 Asp Val Ser Thr Gly Met305          310          315
E--> 1077 320Gln Leu Asn Phe Ser Met Arg Thr Thr Ser Val Phe Pro Asn Met Ala
E--> 1078 325          330          335      Ile Gln Met Thr Ala Ile Gly Glu
      1079 Glu Ser Gly Ser Leu Asp Glu Met          340          345
E--> 1080 350      Leu Ser Lys Val Ala Ser Tyr Tyr Glu Glu Glu Val Asp Asn Ala Val

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E--> 1081 355          360          365          Asp Asn Leu Thr Thr Leu
      1082 Met Glu Pro Met Ile Met Ala Val Leu Gly 370          375
E--> 1083 380          Val Leu Val Gly Gly Leu Ile Val Ala Met Tyr Leu Pro Ile Phe
E--> 1084 Gln385          390          395          400Leu Gly Asn
E--> 1085 Val Val Gly          405
      1087 <210> SEQ ID NO: 43
      1088 <211> LENGTH: 290
      1089 <212> TYPE: PRT
      1090 <213> ORGANISM: Psuedomonas aeruginosa
      1092 <400> SEQUENCE: 43
      1093 Met Pro Leu Leu Asp Tyr Leu Ala Ser His Pro Leu Ala Phe Val Leu 1
E--> 1094 5          10          15          Cys Ala Ile Leu Leu Gly Leu Leu
      1095 Val Gly Ser Phe Leu Asn Val Val          20          25
E--> 1096 30          Val His Arg Leu Pro Lys Met Met Glu Arg Asn Trp Lys Ala Glu Ala
E--> 1097 35          40          45          Arg Glu Ala Leu Gly Leu
      1098 Glu Pro Glu Pro Lys Gln Ala Thr Tyr Asn 50          55
E--> 1099 60          Leu Val Leu Pro Asn Ser Ala Cys Pro Arg Cys Gly His Glu Ile
E--> 1100 Arg65          70          75          80 Pro Trp Glu
      1101 Asn Ile Pro Leu Val Ser Tyr Leu Ala Leu Gly Gly Lys          85
E--> 1102 90          95          Cys Ser Ser Cys Lys Ala Ala Ile Gly Lys Arg Tyr Pro
E--> 1103 Leu Val Glu          100          105          110          Leu
      1104 Ala Thr Ala Leu Leu Ser Gly Tyr Val Ala Trp His Phe Gly Phe          115
E--> 1105 120          125          Thr Trp Gln Ala Gly Ala Met Leu Leu Leu Thr
      1106 Trp Gly Leu Leu Ala 130          135          140
      1107 Met Ser Leu Ile Asp Ala Asp His Gln Leu Leu Pro Asp Val Leu Val145
E--> 1108 150          155          160Leu Pro Leu Leu Trp Leu Gly Leu Ile
      1109 Ala Asn His Phe Gly Leu Phe          165          170
E--> 1110 175          Ala Ser Leu Asp Asp Ala Leu Phe Gly Ala Val Phe Gly Tyr Leu Ser
E--> 1111 180          185          190          Leu Trp Ser Val Phe Trp Leu
      1112 Phe Lys Leu Val Thr Gly Lys Glu Gly          195          200
E--> 1113 205          Met Gly Tyr Gly Asp Phe Lys Leu Leu Ala Met Leu Gly Ala Trp Gly
E--> 1114 210          215          220          Gly Trp Gln Ile Leu
      1115 Pro Leu Thr Ile Leu Leu Ser Ser Leu Val Gly225          230
E--> 1116 235          240Ala Ile Leu Gly Val Ile Met Leu Arg Leu Arg Asn Ala Glu
E--> 1117 Ser Gly          245          250          255          Thr Pro
      1118 Ile Pro Phe Gly Pro Tyr Leu Ala Ile Ala Gly Trp Ile Ala          260
E--> 1119 265          270          Leu Leu Trp Gly Asp Gln Ile Thr Arg Thr Tyr Leu
      1120 Gln Phe Ala Gly          275          280          285
E--> 1121 Phe Lys 290
      1123 <210> SEQ ID NO: 44
      1124 <211> LENGTH: 185
      1125 <212> TYPE: PRT
      1126 <213> ORGANISM: Psuedomonas aeruginosa
      1128 <400> SEQUENCE: 44
      1129 Met Leu Leu Lys Ser Arg His Arg Ser Leu His Gln Ser Gly Phe Ser 1
E--> 1130 5          10          15          Met Ile Glu Val Leu Val Ala Leu
      1131 Leu Leu Ile Ser Ile Gly Val Leu          20          25
E--> 1132 30          Gly Met Ile Ala Met Gln Gly Lys Thr Ile Gln Tyr Thr Ala Asp Ser
E--> 1133 35          40          45          Val Glu Arg Asn Lys Ala

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1134 Ala Met Leu Gly Ser Asn Leu Leu Glu Ser      50                      55
E--> 1135 60          Met Arg Ala Ser Pro Lys Ala Leu Tyr Asp Val Lys Asp Gln Met
E--> 1136 Ala65          70                      75                      80 Thr Gln Ser
1137 Asp Phe Phe Lys Ala Lys Gly Ser Ala Phe Pro Thr Ala                      85
E--> 1138 90          95          Pro Ser Ser Cys Thr Pro Leu Pro Asp Ala Ile Lys Asp
E--> 1139 Arg Leu Gly          100                      105                      110          Cys
1140 Trp Ala Glu Gln Val Lys Asn Glu Leu Pro Gly Ala Gly Asp Leu                      115
E--> 1141 120          125                      Leu Lys Ser Asp Tyr Tyr Ile Cys Arg Ser Ser
1142 Lys Pro Gly Asp Cys          130                      135                      140
1143 Asp Gly Lys Gly Ser Met Leu Glu Ile Arg Leu Ala Trp Arg Gly Lys145
E--> 1144 150          155                      160Gln Gly Ala Cys Val Asn Ala Ala Asp
1145 Ser Ser Ala Asp Thr Ser Leu                      165                      170
E--> 1146 175          Cys Tyr Tyr Thr Leu Arg Val Glu Pro                      180                      185
1148 <210> SEQ ID NO: 45
1149 <211> LENGTH: 274
1150 <212> TYPE: PRT
1151 <213> ORGANISM: Psuedomonas aeruginosa
1153 <400> SEQUENCE: 45
1154 Met Ser Met Asn Asn Arg Ser Arg Arg Gln Ser Gly Leu Ser Met Ile 1
E--> 1155 5          10                      15          Glu Leu Leu Val Ala Leu Ala Ile
1156 Ser Ser Phe Leu Ile Leu Gly Ile                      20                      25
E--> 1157 30          Thr Gln Ile Tyr Leu Asp Asn Lys Arg Asn Tyr Leu Phe Gln Gln Gly
E--> 1158 35          40                      45                      Gln Ala Gly Asn Gln Glu
1159 Asn Gly Arg Phe Ala Met Met Phe Leu Asp          50                      55
E--> 1160 60          Gln Gln Leu Ala Lys Val Gly Phe Arg Arg Arg Ala Asp Asp Pro
E--> 1161 Asn65          70                      75                      80 Glu Phe Ala
1162 Phe Pro Ala Gln Gln Lys Thr Ala Tyr Cys Glu Ala Phe                      85
E--> 1163 90          95          Lys Ala Gly Ser Thr Leu Val Pro Ala Val Val Lys Ala
E--> 1164 Gly Gln Ser          100                      105                      110          Gly
1165 Phe Cys Tyr Arg Tyr Gln Pro Ala Pro Gly Glu Ala Tyr Asp Cys                      115
E--> 1166 120          125                      Glu Gly Asn Ser Ile Thr Thr Pro Ser Asp Pro
1167 Phe Ala Thr Ala Gln          130                      135                      140
1168 Ala Ile Thr Ala Arg Val Leu Phe Val Pro Ala Thr Ala Asp Val Pro145
E--> 1169 150          155                      160Gly Ser Leu Ala Cys Ser Ala Gln Thr
1170 Ile Lys Glu Lys Gly Gln Glu                      165                      170
E--> 1171 175          Ile Val Ser Gly Leu Val Asp Phe Lys Leu Glu Tyr Gly Val Gly Pro
E--> 1172 180          185                      190          Thr Met Ala Gly Lys Arg Glu
1173 Val Glu Ser Phe Val Glu Gln Ala Asn          195                      200
E--> 1174 205          Ile Ala Asp Arg Pro Val Arg Ala Leu Arg Tyr Ser Ala Leu Met Ala
E--> 1175 210          215                      220          Ser Asp Lys Asn Leu
1176 Arg Gln Gly Asp Ser Lys Thr Leu Asp Asp Trp225
E--> 1177 235          240Ile Thr Leu Tyr Pro Ser Ser Lys Thr Ser Leu Gln Gly Asn
E--> 1178 Asp Lys          245                      250                      255          Asp Arg
1179 Leu Tyr Gln Ile Ala Lys Gly Ser Gln Thr Leu Arg Asn Leu                      260
E--> 1180 265          270          Val Pro
1182 <210> SEQ ID NO: 46
1183 <211> LENGTH: 172
1184 <212> TYPE: PRT
1185 <213> ORGANISM: Psuedomonas aeruginosa

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1187 <400> SEQUENCE: 46
1188 Met Asn Asn Phe Pro Ala Gln Gln Arg Gly Ala Thr Leu Val Ile Ala 1
E--> 1189 5          10          15          Leu Ala Ile Leu Val Ile Val Thr
1190 Leu Leu Ala Val Ser Ser Met Arg          20          25
E--> 1191 30          Glu Val Val Leu Glu Ser Arg Ile Thr Gly Asn Val Ile Glu Gln Thr
E--> 1192 35          40          45          Arg Leu Gln Asn Ala Ala
1193 Glu Ser Gly Leu Arg Glu Gly Glu Arg Arg          50          55
E--> 1194 60          Phe Val Asn Thr Leu Arg Pro Pro Glu Pro Gly Thr Gly Cys Thr
E--> 1195 Ala65          70          75          80 Asp Asn Val
1196 Ala Arg Pro Cys Leu Leu Asp Leu Ala Ala Leu Asn Leu          85
E--> 1197 90          95          Lys Leu Ala Asp Thr His Gln Asn Pro Val Gly Val Leu
E--> 1198 Lys Gly Ile          100          105          110          Ala
1199 Asn Thr Trp Met Ser Tyr Arg Gly Ser Asp Ile Ser Ser Ala Thr          115
E--> 1200 120          125          Thr Ala Gly Asn Ala Leu Gln Arg Ala Val Glu
1201 Gln Pro Ala His Ser          130          135          140
1202 Leu Gly Arg Pro Gly Gln Arg Ser Gly Lys Pro Arg Ile Arg Gln Pro145
E--> 1203 150          155          160Asp Ala Arg His Arg His Leu Leu Leu
E--> 1204 Arg Asp Gln          165          170
1206 <210> SEQ ID NO: 47
1207 <211> LENGTH: 1161
1208 <212> TYPE: PRT
1209 <213> ORGANISM: Psuedomonas aeruginosa
1211 <400> SEQUENCE: 47
1212 Met Arg Gly Ile Gly Thr Phe Tyr Tyr Glu Thr Asn Ser Val Ala Arg 1
E--> 1213 5          10          15          Asn Gln Thr Asn Ser Glu Thr Val
1214 Leu Gln Thr Val Ala Arg Pro Ser          20          25
E--> 1215 30          Leu Tyr Gln Leu Ile Glu Pro Arg Met Lys Ser Val Leu His Gln Ile
E--> 1216 35          40          45          Gly Lys Thr Ser Leu Ala
1217 Ala Ala Leu Ser Gly Ala Val Leu Leu Ser          50          55
E--> 1218 60          Ala Gln Thr Thr His Ala Ala Ala Leu Ser Val Ser Gln Gln Pro
E--> 1219 Leu65          70          75          80 Met Leu Ile
1220 Gln Gly Val Ala Pro Asn Met Leu Val Thr Leu Asp Asp          85
E--> 1221 90          95          Ser Gly Ser Met Ala Phe Ala Tyr Ala Pro Asp Ser Ile
E--> 1222 Ser Gly Tyr          100          105          110          Gly
1223 Asn Tyr Thr Phe Phe Ala Ser Asn Ser Phe Asn Pro Met Tyr Phe          115
E--> 1224 120          125          Asp Pro Asn Thr Gln Tyr Lys Leu Pro Lys Lys
1225 Leu Thr Leu Val Asn          130          135          140
1226 Gly Gln Val Gln Ile Gln Asp Tyr Pro Ala Pro Asn Phe Ser Ser Ala145
E--> 1227 150          155          160Trp Arg Asn Gly Phe Thr Arg Arg Gly
1228 Ser Ile Asn Leu Ser Asn Ser          165          170
E--> 1229 175          Tyr Lys Val Thr Ile Glu Tyr Gly Arg Gly Tyr Asp Lys Glu Ser Thr
E--> 1230 180          185          190          Ile Lys Ala Asp Ala Ala Tyr
1231 Tyr Tyr Asp Phe Thr Gly Ser Ser Ser          195          200
E--> 1232 205          Trp Asn Arg Thr Asn Gln Ala Cys Tyr Thr Arg Arg Tyr Val Ser Thr
E--> 1233 210          215          220          Glu Gln Arg Gln Asn
1234 Phe Ala Asn Trp Tyr Ser Phe Tyr Arg Thr Arg225          230
E--> 1235 235          240Ala Leu Arg Thr Gln Thr Ala Ala Asn Leu Ala Phe Phe Arg
E--> 1236 Leu Pro          245          250          255          Glu Asn
1237 Ala Arg Val Ser Trp Gln Leu Leu Asn Asp Ser Asn Cys Asn          260

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E--> 1238 265          270      Gln Met Gly Ser Gly Ser Arg Leu Arg Gln Leu Phe
      1239 Gln Gln Leu Ser          275          280          285
      1240 Thr Gly Leu His Arg Ser Thr Ala Gly Glu Leu Leu Gln Leu Ala Gly 290
E--> 1241 295          300      Lys Thr Phe Gly Gln Trp Trp Tyr Ala Leu
      1242 Arg Gln Ala Met Thr Arg305          310          315
E--> 1243 320Glu Ala Ser Phe Ser Arg Arg Pro Ala Ser Asn Gly Pro Tyr Ala Tyr
E--> 1244 325          330          335      Arg Pro Gly Thr Gln Thr Ala Pro
      1245 Glu Tyr Ser Cys Arg Gly Ser Tyr          340          345
E--> 1246 350      His Ile Leu Met Thr Asp Gly Leu Trp Asn Asn Asp Ser Ala Asn Val
E--> 1247 355          360          365          Gly Asn Ala Asp Ser Thr
      1248 Ala Arg Asn Leu Pro Asp Gly Lys Ser Tyr          370          375
E--> 1249 380      Ser Ser Gln Thr Pro Tyr Arg Asp Gly Thr Phe Asp Thr Leu Ala
E--> 1250 Asp385          390          395          400Gln Ala Phe
      1251 His Tyr Trp Ala Thr Asp Ala Arg Pro Asp Ile Asp Asp          405
E--> 1252 410          415      Asn Ile Lys Pro Tyr Ile Pro Tyr Pro Asp Gln Asp Asn
E--> 1253 Pro Ser Gly          420          425          430          Glu
      1254 Tyr Trp Asn Pro Arg Asn Asp Pro Ala Ile Trp Gln His Met Val          435
E--> 1255 440          445      Thr Tyr Thr Leu Gly Leu Gly Leu Asn Thr Ser
      1256 Leu Thr Ser Pro Arg          450          455          460
      1257 Trp Glu Gly Ser Thr Phe Ser Gly Gly Tyr Asn Asp Ile Val Ala Gly465
E--> 1258 470          475          480Asn Leu Ser Trp Pro Arg Ala Ser Asn
      1259 Asn Asp Ser Asn Asn Val Tyr          485          490
E--> 1260 495      Asp Leu Trp His Ala Ala Val Asn Ser Arg Gly Glu Phe Phe Ser Ala
E--> 1261 500          505          510      Asp Ser Pro Asp Gln Leu Val
      1262 Ala Ala Phe Gln Asp Ile Leu Asn Arg          515          520
E--> 1263 525      Ile Ser Gly Lys Asp Leu Pro Ala Ser Arg Pro Ala Ile Ser Ser Ser
E--> 1264 530          535          540          Leu Gln Glu Asp Asp
      1265 Thr Gly Asp Lys Leu Thr Arg Phe Ala Tyr Gln545          550
E--> 1266 555          560Thr Ser Phe Ala Ser Asp Lys Asn Trp Ala Gly Asp Leu Thr
E--> 1267 Arg Tyr          565          570          575      Ser Leu
      1268 Thr Thr Gln Asp Lys Ala Thr Val Gln Thr Asn Leu Trp Ser          580
E--> 1269 585          590      Ala Gln Ser Ile Leu Asp Ala Met Pro Asn Gly Gly
      1270 Ala Gly Arg Lys          595          600          605
      1271 Ile Met Met Ala Gly Ser Gly Thr Ser Gly Leu Lys Glu Phe Thr Trp          610
E--> 1272 615          620          Gly Ser Leu Ser Ala Asp Gln Gln Arg Lys
      1273 Leu Asn Arg Asp Pro Asp625          630          635
E--> 1274 640Arg Asn Asp Val Ala Asp Thr Lys Gly Gln Asp Arg Val Ala Phe Leu
E--> 1275 645          650          655      Arg Gly Asp Arg Arg Lys Glu Asn
      1276 Ser Asp Asn Phe Arg Thr Arg Asn          660          665
E--> 1277 670      Ser Ile Leu Gly Asp Ile Ile Asn Ser Ser Pro Ala Thr Val Gly Lys
E--> 1278 675          680          685          Ala Gln Tyr Leu Thr Tyr
      1279 Leu Ala Gln Pro Ile Glu Pro Ser Gly Asn          690          695
E--> 1280 700      Tyr Ser Thr Phe Ala Glu Ala Gln Lys Thr Arg Ala Pro Arg Val
E--> 1281 Tyr705          710          715          720Val Gly Ala
      1282 Asn Asp Gly Met Leu His Gly Phe Asp Thr Asp Gly Asn          725
E--> 1283 730          735      Glu Thr Phe Ala Phe Ile Pro Ser Ala Val Phe Glu Lys
E--> 1284 Leu His Lys          740          745          750          Leu
      1285 Thr Ala Arg Gly Tyr Gln Gly Gly Ala His Gln Phe Tyr Val Asp          755
E--> 1286 760          765      Gly Ser Pro Val Val Ala Asp Ala Phe Phe Gly

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1287 Gly Ala Trp His Thr      770              775              780
1288 Val Leu Ile Gly Ser Leu Arg Ala Gly Gly Lys Gly Leu Phe Ala Leu785
E--> 1289 790              795              800Asp Val Thr Asp Pro Ala Asn Ile Lys
1290 Leu Leu Trp Glu Ile Gly Val              805              810
E--> 1291 815      Asp Gln Glu Pro Asp Leu Gly Tyr Ser Phe Pro Lys Pro Thr Val Ala
E--> 1292 820              825              830      Arg Leu His Asn Gly Lys Trp
1293 Ala Val Val Thr Gly Asn Gly Tyr Ser              835              840
E--> 1294 845              Ser Leu Asn Asp Lys Ala Ala Leu Leu Ile Ile Asp Leu Glu Thr Gly
E--> 1295 850              855              860              Ala Ile Thr Arg Lys
1296 Leu Glu Val Thr Gly Arg Thr Gly Val Pro Asn865              870
E--> 1297 875              880Gly Leu Ser Ser Leu Arg Leu Ala Asp Asn Asn Ser Asp Gly
E--> 1298 Val Ala              885              890              895      Asp Tyr
1299 Ala Tyr Ala Gly Asp Leu Gln Gly Asn Leu Trp Arg Phe Asp              900
E--> 1300 905              910      Leu Ile Ala Gly Lys Val Asn Gln Asp Asp Pro Phe
1301 Ser Arg Ala Asn              915              920              925
1302 Asp Gly Pro Thr Val Ala Ser Ser Phe Arg Val Ser Phe Gly Gly Gln              930
E--> 1303 935              940              Pro Leu Tyr Ser Ala Val Asp Ser Ala Gly
1304 Ala Ala Gln Ala Ile Thr945              950              955
E--> 1305 960Ala Ala Pro Ser Leu Val Arg His Pro Thr Arg Lys Gly Tyr Ile Val
E--> 1306 965              970              975      Ile Phe Gly Thr Gly Lys Tyr Phe
1307 Glu Asn Ala Asp Ala Arg Ala Asp              980              985
E--> 1308 990      Thr Ser Arg Ala Gln Thr Leu Tyr Gly Ile Trp Asp Gln Gln Thr Lys
E--> 1309 995              1000              1005      Gly Glu Ala Ala Gly Ser
1310 Thr Pro Arg Leu Thr Arg Gly Asn Leu Gln              1010              1015
E--> 1311 1020      Gln Gln Thr Leu Asp Leu Gln Ala Asp Ser Thr Phe Ala Ser Thr
E--> 1312 Ala1025              1030              1035              104Arg Thr Ile
1313 Arg Ile Gly Ser Gln Asn Pro Val Asn Trp Leu Asn Asn              1045
E--> 1314 1050              1055      Asp Gly Ser Thr Lys Gln Ser Gly Trp Tyr Leu Asp Phe
E--> 1315 Met Val Asn              1060              1065              1070      Gly
1316 Thr Leu Lys Gly Glu Met Leu Ile Glu Asp Met Ile Ala Ile Gly              1075
E--> 1317 1080              1085      Gln Val Val Leu Leu Gln Thr Ile Thr Pro Asn
1318 Asp Asp Pro Cys Ala              1090              1095              1100
1319 Asp Gly Ala Ser Asn Trp Thr Tyr Gly Leu Asp Pro Tyr Thr Gly Gly1105
E--> 1320 1110              1115              112Arg Thr Arg Phe Thr Val Phe Asp Leu
1321 Gly Arg Gln Gly Val Val Gly              1125              1130
E--> 1322 1135      Leu Glu Ile Arg Leu Thr Gly Thr Thr Arg Arg Asn Val Gly Asn Pro
E--> 1323 1140              1145              1150      Val Pro Ser Arg Lys Ala Trp
E--> 1324 Glu Ala              1155              1160

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Input Set : A:\Ep.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
 L:33 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:34 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:35 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:36 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:37 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:37 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:38 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:44 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 L:49 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
 M:254 Repeated in SeqNo=1
 L:50 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:50 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1090 Found:70 SEQ:1
 L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:63 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
 L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2

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L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 M:254 Repeated in SeqNo=2
 L:67 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:67 M:252 E: No. of Seq. differs, <211>LENGTH:Input:277 Found:97 SEQ:2
 L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
 L:81 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:82 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:83 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:84 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:85 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:86 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:87 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:90 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 M:254 Repeated in SeqNo=3
 L:93 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:93 M:252 E: No. of Seq. differs, <211>LENGTH:Input:819 Found:99 SEQ:3
 L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:106 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:4
 L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:110 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:111 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:112 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6

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L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:113 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:114 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:115 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:116 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:117 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 L:118 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
 L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
 M:254 Repeated in SeqNo=4
 L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:119 M:252 E: No. of Seq. differs, <211>LENGTH:Input:832 Found:112 SEQ:4
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:132 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:5
 L:133 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:134 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:135 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:136 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
 L:138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:6
 L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5.
 L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 M:254 Repeated in SeqNo=5
 L:149 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
 L:149 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1054 Found:94 SEQ:5
 L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 L:162 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:6
 L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
 M:254 Repeated in SeqNo=6
 L:176 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:176 M:252 E: No. of Seq. differs, <211>LENGTH:Input:880 Found:100 SEQ:6
 L:189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 L:189 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
 L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
 M:254 Repeated in SeqNo=7
 L:201 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:201 M:252 E: No. of Seq. differs, <211>LENGTH:Input:779 Found:119 SEQ:7
 L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:214 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:8

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L:228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
M:254 Repeated in SeqNo=8
L:228 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:228 M:252 E: No. of Seq. differs, <211>LENGTH:Input:848 Found:68 SEQ:8
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:241 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:9
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
M:254 Repeated in SeqNo=9
L:249 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:249 M:252 E: No. of Seq. differs, <211>LENGTH:Input:533 Found:113 SEQ:9
L:262 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:10
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
M:254 Repeated in SeqNo=10
L:271 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:271 M:252 E: No. of Seq. differs, <211>LENGTH:Input:591 Found:111 SEQ:10
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:284 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
M:254 Repeated in SeqNo=11
L:304 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:304 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1249 Found:109 SEQ:11
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:12
M:254 Repeated in SeqNo=12
L:323 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:323 M:252 E: No. of Seq. differs, <211>LENGTH:Input:373 Found:73 SEQ:12
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
M:254 Repeated in SeqNo=13
L:347 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:347 M:252 E: No. of Seq. differs, <211>LENGTH:Input:683 Found:83 SEQ:13
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:360 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
M:254 Repeated in SeqNo=14
L:371 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:371 M:252 E: No. of Seq. differs, <211>LENGTH:Input:672 Found:72 SEQ:14
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:384 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
L:411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
M:254 Repeated in SeqNo=15
L:411 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:411 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1676 Found:116 SEQ:15
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:424 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:16
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
M:254 Repeated in SeqNo=16
L:435 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:436 M:252 E: No. of Seq. differs, <211>LENGTH:Input:721 Found:121 SEQ:16

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L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:449 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
 L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 M:254 Repeated in SeqNo=17
 L:456 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:456 M:252 E: No. of Seq. differs, <211>LENGTH:Input:452 Found:92 SEQ:17
 L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 L:469 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
 L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
 M:254 Repeated in SeqNo=18
 L:476 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:476 M:252 E: No. of Seq. differs, <211>LENGTH:Input:442 Found:82 SEQ:18
 L:489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 L:489 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
 L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
 M:254 Repeated in SeqNo=19
 L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:497 M:252 E: No. of Seq. differs, <211>LENGTH:Input:538 Found:118 SEQ:19
 L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 L:510 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
 L:513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
 M:254 Repeated in SeqNo=20
 L:513 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:513 M:252 E: No. of Seq. differs, <211>LENGTH:Input:218 Found:98 SEQ:20
 L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
 L:526 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:21
 L:536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
 M:254 Repeated in SeqNo=21
 L:536 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:536 M:252 E: No. of Seq. differs, <211>LENGTH:Input:642 Found:102 SEQ:21
 L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 L:549 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:22
 L:558 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
 M:254 Repeated in SeqNo=22
 L:558 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:558 M:252 E: No. of Seq. differs, <211>LENGTH:Input:583 Found:103 SEQ:22
 L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 L:571 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:23
 L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
 M:254 Repeated in SeqNo=23
 L:576 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:576 M:252 E: No. of Seq. differs, <211>LENGTH:Input:360 Found:120 SEQ:23
 L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
 L:589 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:24
 L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
 M:254 Repeated in SeqNo=24
 L:597 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
 L:597 M:252 E: No. of Seq. differs, <211>LENGTH:Input:494 Found:74 SEQ:24
 L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26

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L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:693 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:695 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
L:695 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=34
L:696 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:698 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:699 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:699 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:701 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:707 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:715 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:723 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:730 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:730 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:738 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:746 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:749 M:252 E: No. of Seq. differs, <211>LENGTH:Input:595 Found:328 SEQ:34
L:758 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:760 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:760 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=35
L:761 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:763 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:764 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:764 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:766 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:768 M:252 E: No. of Seq. differs, <211>LENGTH:Input:119 Found:66 SEQ:35
L:777 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:779 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:779 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=36
L:780 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:782 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:783 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:783 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:785 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:791 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:799 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:804 M:252 E: No. of Seq. differs, <211>LENGTH:Input:295 Found:158 SEQ:36
L:813 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
L:815 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=37
L:816 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:818 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:819 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:819 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:821 M:333 E: Wrong sequence grouping, Amino acids not in groups!

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Output Set: N:\CRF3\02272002\I673605.raw

L:827 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:835 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:841 M:252 E: No. of Seq. differs, <211>LENGTH:Input:308 Found:158 SEQ:37
 L:850 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:852 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
 L:852 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=38
 L:853 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:855 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:856 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:856 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:858 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:864 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:872 M:252 E: No. of Seq. differs, <211>LENGTH:Input:245 Found:129 SEQ:38
 L:881 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:883 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
 L:883 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 M:332 Repeated in SeqNo=39
 L:884 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:886 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:887 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:887 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:889 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:895 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:903 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:911 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:916 M:252 E: No. of Seq. differs, <211>LENGTH:Input:375 Found:213 SEQ:39
 L:927 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
 M:332 Repeated in SeqNo=40
 L:931 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:962 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:976 M:252 E: No. of Seq. differs, <211>LENGTH:Input:547 Found:306 SEQ:40
 L:987 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
 M:332 Repeated in SeqNo=41
 L:991 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1022 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1038 M:252 E: No. of Seq. differs, <211>LENGTH:Input:566 Found:311 SEQ:41
 L:1049 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
 M:332 Repeated in SeqNo=42
 L:1053 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1084 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1085 M:252 E: No. of Seq. differs, <211>LENGTH:Input:406 Found:231 SEQ:42
 L:1096 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
 M:332 Repeated in SeqNo=43
 L:1100 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
 L:1121 M:252 E: No. of Seq. differs, <211>LENGTH:Input:290 Found:158 SEQ:43
 L:1132 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
 M:332 Repeated in SeqNo=44
 L:1136 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

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Input Set : A:\Ep.txt

Output Set: N:\CRF3\02272002\I673605.raw

L:1146 M:252 E: No. of Seq. differs, <211>LENGTH:Input:185 Found:85 SEQ:44
L:1157 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
M:332 Repeated in SeqNo=45
L:1161 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1180 M:252 E: No. of Seq. differs, <211>LENGTH:Input:274 Found:148 SEQ:45
L:1191 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1195 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1204 M:252 E: No. of Seq. differs, <211>LENGTH:Input:172 Found:85 SEQ:46
L:1215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
M:332 Repeated in SeqNo=47
L:1219 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1250 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1281 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1312 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1324 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1161 Found:654 SEQ:47
L:1335 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:48
M:332 Repeated in SeqNo=48
L:1339 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1343 M:252 E: No. of Seq. differs, <211>LENGTH:Input:115 Found:66 SEQ:48

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001
<141> 1998-12-31

<150> US 08/999,999
<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1
<211> 389
<212> DNA
<213> Paramecium sp.

<220>
<221> CDS
<222> (279)...(389)

<300>
<301> Doc, Richard
<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.
<303> Journal of Genes
<304> 1
<305> 4
<306> 1-7
<307> 1988-06-31
<308> 123456
<309> 1988-06-31

<400> 1
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tgatgtggca attgctggca gtgccacagg cttttcagcc aggcttaggg tgggttcgcg 180
cgcggcgcgg cggccctctt cgcgctcttc tcgcgcctct ctctcgtctt cctctcgtct 240

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ggacctgatt	aggtgagcag	gaggagggggg	cagtttagc	atg	gtt	tca	atg	ttc	agc	296
				Met	Val	Ser	Met	Phe	Ser	
				1				5		
ttg	tct	ttc	aaa	tgg	cct	gga	ttt	tgt	ttg	344
Leu	Ser	Phe	Lys	Trp	Pro	Gly	Phe	Cys	Leu	
			10					15	20	
tgt	ccc	aaa	gtc	ctc	ccc	tgt	cac	tca	tca	389
Cys	Pro	Lys	Val	Leu	Pro	Cys	His	Ser	Ser	
		25					30			
<210>		2								
<211>		37								
<212>		PRT								
<213>		Paramecium sp.								
<<400>		2								
Met	Val	Ser	Met	Phe	Ser	Leu	Ser	Phe	Lys	344
1				5					10	
Phe	Val	Cys	Leu	Phe	Gln	Cys	Pro	Lys	Val	389
			20					25		
Leu	Gln	Pro	Asn	Leu						
		35								
<210>		3								
<211>		11								
<212>		PRT								
<213>		Artificial Sequence								
<220>										
<223>										
<400>		3								
Met	Val	Asn	Leu	Glu	Pro	Met	His	Thr	Glu	344
1				5					10	
<210>		4								
<400>		4								
000										

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOS	Count includes total number of SEQ ID NOS	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	0
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	0
<313>	Relevant Residues	FROM (position) TO (position)	0
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	0

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;